

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 19:58:50 ; Search time 125 Seconds
(without alignments)
83.540 Million cell updates/sec

Title: US-10-627-685a-1

Perfect score: 120

Sequence: 1 CXIXNQXCXQLDDCCSXXCNXXKCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	27	2	AAW35723 Kappa-con
2	120	100.0	27	4	AAU10200 Snail Kap
3	120	100.0	27	4	AAU10195 Snail Kap
4	120	100.0	27	4	AAU10208 Snail Kap
5	120	100.0	27	4	AAU10205 Snail Kap
6	120	100.0	27	4	AAU10199 Snail Kap
7	120	100.0	27	4	AAU10196 Snail Kap
8	120	100.0	27	4	AAU10202 Snail Kap
9	120	100.0	27	4	AAU10197 Snail Kap
10	120	100.0	27	4	AAU10206 Snail Kap
11	120	100.0	27	4	AAU10207 Snail Kap
12	120	100.0	27	4	AAU10201 Snail Kap
13	120	100.0	27	4	AAU10204 Snail Kap
14	120	100.0	27	4	AAU10218 Snail Kap
15	120	100.0	27	4	AAU10203 Snail Kap
16	120	100.0	27	6	AAE38342 Conus pur
17	120	100.0	27	6	AAE38344 Conus pur
18	120	100.0	27	6	AAE38336 Conus pur
19	120	100.0	27	6	AAE38339 Conus pur
20	120	100.0	27	6	AAE38345 Conus pur
21	120	100.0	27	6	AAE38337 Conus pur
22	120	100.0	27	6	AAE38340 Conus pur
23	120	100.0	27	6	AAE38335 Conus pur
24	120	100.0	27	6	AAE38346 Conus pur
25	120	100.0	27	6	AAE38343 Conus pur

26	120	100.0	27	6	AAE38358 Conus pur
27	120	100.0	27	6	AAE38341 Conus pur
28	120	100.0	27	6	AAE38347 Conus pur
29	120	100.0	27	6	AAE38348 Conus pur
30	117	97.5	27	4	AAU10212 Snail Kap
31	117	97.5	27	6	AAE38352 Conus pur
32	116	96.7	27	4	AAU10217 Snail Kap
33	116	96.7	27	6	AAE38357 Conus pur
34	115	95.8	27	4	AAU10214 Snail Kap
35	115	95.8	27	4	AAU10198 Snail Kap
36	115	95.8	27	6	AAE38338 Conus pur
37	115	95.8	27	6	AAE38354 Conus pur
38	114	95.0	27	4	AAU10216 Snail Kap
39	114	95.0	27	4	AAU10210 Snail Kap
40	114	95.0	27	6	AAE38356 Conus pur
41	114	95.0	27	6	AAE38350 Conus pur
42	112	93.3	27	4	AAU10213 Snail Kap
43	112	93.3	27	4	AAU10209 Snail Kap
44	112	93.3	27	4	AAU10219 Snail Kap
45	112	93.3	27	4	AAU10215 Snail Kap
46	112	93.3	27	4	AAU10211 Snail Kap
47	112	93.3	27	6	AAE38353 Conus pur
48	112	93.3	27	6	AAE38351 Conus pur
49	112	93.3	27	6	AAE38355 Conus pur
50	112	93.3	27	6	AAE38349 Conus pur
51	112	93.3	27	6	AAE38359 Conus pur
52	81	67.5	26	2	AAE38358 Conus pur
53	81	67.5	26	2	AAE38357 Conus pur
54	81	67.5	26	2	AAE38356 Conus pur
55	81	67.5	26	2	AAE38355 Conus pur
56	81	67.5	26	2	AAE38354 Conus pur
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58	81	67.5	26	3	AAE38352 Conus pur
59	81	67.5	26	3	AAE38351 Conus pur
60	81	67.5	26	4	AAE38350 Conus pur
61	81	67.5	26	5	AAE38349 Conus pur
62	81	67.5	26	5	AAE38348 Conus pur
63	77	64.2	26	2	AAE38347 Conus pur
64	77	64.2	26	2	AAE38346 Conus pur
65	77	64.2	26	2	AAE38345 Conus pur
66	77	64.2	26	2	AAE38344 Conus pur
67	77	64.2	26	2	AAE38343 Conus pur
68	77	64.2	26	2	AAE38342 Conus pur
69	77	64.2	26	3	AAE38341 Conus pur
70	77	64.2	26	4	AAE38340 Conus pur
71	77	64.2	26	4	AAE38339 Conus pur
72	77	64.2	26	4	AAE38338 Conus pur
73	77	64.2	26	5	AAE38337 Conus pur
74	74	61.7	26	5	AAE38336 Conus pur
75	72	60.0	26	5	AAE38335 Conus pur
76	70	58.3	26	5	AAE38334 Conus pur
77	69	57.5	26	5	AAE38333 Conus pur
78	69	57.5	26	2	AAE38332 Conus pur
79	69	57.5	26	2	AAE38331 Conus pur
80	69	57.5	26	2	AAE38330 Conus pur
81	69	57.5	26	2	AAE38329 Conus pur
82	69	57.5	26	2	AAE38328 Conus pur
83	69	57.5	26	2	AAE38327 Conus pur
84	69	57.5	26	2	AAE38326 Conus pur
85	69	57.5	26	2	AAE38325 Conus pur
86	69	57.5	26	2	AAE38324 Conus pur
87	69	57.5	26	3	AAE38323 Conus pur
88	69	57.5	26	3	AAE38322 Conus pur
89	69	57.5	26	3	AAE38321 Conus pur
90	69	57.5	26	3	AAE38320 Conus pur
91	69	57.5	26	3	AAE38319 Conus pur
92	69	57.5	26	4	AAE38318 Conus pur
93	69	57.5	26	4	AAE38317 Conus pur
94	69	57.5	26	4	AAE38316 Conus pur
95	69	57.5	26	5	AAE38315 Conus pur
96	69	57.5	26	5	AAE38314 Conus pur
97	69	57.5	26	5	AAE38313 Conus pur
98	68.5	57.1	342	8	ADP04517 Sea equir

99 68 56.7 2444 5 ABB07821 Abb07821 Constitut
100 68 56.7 2444 5 ADI16933 ADI16933 Human NOV

ALIGNMENTS

RESULT 1
AAW35723
ID AAW35723 standard; peptide; 27 AA.
XX AC AAW35723;
XX DT 03-APR-1998 (first entry)
XX DE Kappa-conotoxin PVIIA.
XX KW Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;
XX KW cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Disulfide-bond 1..16
FT /note= "disulphide bond"
FT Modified-site 4
FT /note= "Optionally 4-trans-hydroxyproline, hydroxyproline
or proline"
FT Disulfide-bond 8..20
FT /note= "disulphide bond"
FT Disulfide-bond 15..26
FT /note= "disulphide bond"
XX W09734925-A1.
XX 25-SEP-1997.
XX 14-MAR-1997; 97WO-US003483.
XX 18-MAR-1996; 96US-00619936.
XX (UTAH) UNIV UTAH RES FOUND.
XX Terlau H, Shon K, Grille MM, Olivera BM;
XX WPI; 1997-480162/44.
XX New kappa-conotoxin peptides - which target potassium channels and can be
XX used to augment neurotransmitter release in e.g. autoimmune diseases.
XX Claim 1; Page 23; 29pp; English.
XX The present sequence represents a new kappa-conotoxin PVIIA which targets
XX potassium channels and can be used to augment neurotransmitter release in
XX pathological situations such as autoimmune diseases, e.g. Alzheimer's
XX disease, Lambert-Eaton syndrome or myasthenia gravis. This peptide
XX together with delta-conotoxin PVIIA act synergistically to rapidly
XX immobilize fish which are injected with the two peptides. Injection of
XX kappa-conotoxin PVIIA alone results in different symptoms with an
XX injected fish becoming hyperactive and then contracting and suddenly
XX extending all major fins. This "fin-popping" occurs repeatedly resulting
XX in a series of jerky movements, but injection of only kappa-conotoxin
XX PVIIA does not immobilize or kill the fish
SQ Sequence 27 AA;
Query Match 100.0%; Score 120; DB 2; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00084;
Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
Db 1 CRIPNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 2
AAU10200
ID AAU10200 standard; peptide; 27 AA.
XX AC AAU10200;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R2A.
XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
XX KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
XX KW cerebral ischaemia; ocular ischaemia; asthma; R2A.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
amide group"
XX W0200121648-A1.
XX 29-MAR-2001.
XX 21-SEP-2000; 2000WO-US025827.
XX 22-SEP-1999; 99US-0155135P.
XX 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX Claim 1; Page 27; 46pp; English.
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX PVIIA) peptide or its analogue, derivative or physiologically active
XX salt. The conotoxins are used for treating disorders associated with
XX radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 100.0%; Score 120; DB 4; Length 27;
Best Local Similarity 66.7%; Pred. No. 0.00084;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
Db 1 CALXNQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 3
AAU10195
ID AAU10195 standard; peptide; 27 AA.

XX AC AAU10195;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue #1.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma.
 XX OS Conus purpurascens.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Misc-difference 2
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 4
 FT /label= OTHER
 FT /note= "Other= Pro or Hydroxyproline"
 FT Misc-difference 7
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 9
 FT /label= OTHER
 FT /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 FT mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
 FT nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
 FT Misc-difference 11
 FT /label= OTHER
 FT /note= "Other= His or halo-His"
 FT Misc-difference 18
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 19
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 22
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Misc-difference 23
 FT /label= OTHER
 FT /note= "Other= Phe, Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
 FT mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
 FT nitro-Tyr, (D,L)-Trp, neo-Trp or (D,L)-halo-Trp"
 FT Misc-difference 25
 FT /label= OTHER
 FT /note= "Other= Arg, homoArg, ornithine, Lys, N-methyl-
 FT Lys, N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any synthetic
 FT basic amino acid, His or halo-His"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;
 XX WPI; 2001-648090/74.
 XX Treating disorders associated with radical depolarization of excitable
 FT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises
 FT activating a KATP channel by administering to an individual a kappa-
 FT conotoxin PVIIA peptide.
 XX Claim 1; Page 27; 46pp; English.
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 0.00084;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CXIXNOXCXQXLDCCSXCNXXNXXCV 27
 Db 1 CXIXNOXCXQXLDCCSXCNXXNXXCV 27
 RESULT 4
 AAU10208
 ID AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX Snail Kappa-conotoxin PVIIA analogue H11A.
 DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H11A.
 XX OS Conus purpurascens.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 4
 FT /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX WO200121648-A1.
 XX 29-MAR-2001.
 XX 21-SEP-2000; 2000WO-US025827.
 XX 22-SEP-1999; 99US-0155135P.
 XX 20-JUL-2000; 2000US-0219438P.
 XX (COGN-) COGNETIX INC.
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 XX Jones RR;

Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

[illegible]

XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX WPI; 2003-679464/64.
 DR
 XX
 XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 PS Disclosure; Page 7; 32pp; English.
 XX
 XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXCNXXKVCV 27
 Db 1 CRIPNQCFQHLDDCCSRKCNRFKVCV 27
 RESULT 18
 AAE38336
 ID AAE38336 standard; peptide; 27 AA.
 AC AAE38336;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, R18A.
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT
 XX WO2003063782-A2.
 XX
 PD 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US0002384.
 XX
 XX 29-JAN-2002; 2002US-0352219P.
 XX
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

PI Olivera BM;
 XX WPI; 2003-679464/64.
 XX
 PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
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 PS Disclosure; Page 6; 32pp; English.
 XX
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 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;
 Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQXLDCCSXCNXXKVCV 27
 Db 1 CRIPNQCFQHLDDCCSRKCNRFKVCV 27
 RESULT 19
 AAE38339
 ID AAE38339 standard; peptide; 27 AA.
 AC AAE38339;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, K19A.
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT
 XX WO2003063782-A2.
 XX
 PD 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US0002384.
 XX
 XX 29-JAN-2002; 2002US-0352219P.
 XX
 XX (COGN-) COGNETIX INC.
 PA (UTAH) UNIV UTAH RES FOUND.
 XX
 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX WPI; 2003-679464/64.
 XX
 XX Protection and preservation of an organ e.g. heart of a mammal comprises

PT use of a compound binding to kappa-PVIIA-binding site.

PS Disclosure; Page 7; 32pp; English.

CC The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide

XX Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;

Best Local Similarity 63.0%; Pred. No. 0.00084;

Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXINQXCXQXLDCCSXKCNXXKVCV 27

Db 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27

RESULT 20

AAE38345
ID AAE38345 standard; peptide; 27 AA.

AC AAE38345;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, P9M.

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers

FT Modified-site 4

FT /label= Hyp

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as

CC organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue peptide

XX Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;

Best Local Similarity 63.0%; Pred. No. 0.00084;

Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXINQXCXQXLDCCSXKCNXXKVCV 27

Db 1 CRIPNOKCFQHLDDCCSRKCNRFNKCV 27

RESULT 21

AAE38337
ID AAE38337 standard; peptide; 27 AA.

AC AAE38337;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, R22A.

Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers

FT Modified-site 4

FT /label= Hyp

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 6; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury,

The invention relates to kappa-PVIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present

FT	D or L-Trp, neo-Trp, D or L-halo-Trp or any synthetic aromatic amino acid; preferably Phe"
FT	Misc-difference 25
FT	/label= Arg, Orn, Lys, His, OTHER
FT	/note= "OTHER = Homo-Arg, N-methyl-Lys, N-N-dimethyl-Lys, N-N-N-trimethyl-Lys, any synthetic basic amino acid, halo
FT	-His; preferably Lys"
XX	
PN	WO2003063782-A2.
XX	
PD	07-AUG-2003.
XX	
PF	28-JAN-2003; 2003WO-US002384.
XX	
PR	29-JAN-2002; 2002US-0352219P.
XX	
PA	(COGN-) COGNETIX INC.
PA	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI	Oliviera BW;
XX	
DR	WPI; 2003-679464/64.
XX	
PT	Protection and preservation of an organ e.g. heart of a mammal comprises use of a compound binding to kappa-PVIIA-binding site.
PT	
PS	Disclosure; Page 5; 32pp; English.
XX	
CC	The invention relates to kappa-PVIIA-related conotoxins and their use as organ protectants. The invention also relates to a method of arresting, protecting and/or preserving an organ of a mammal using kappa-PVIIA-related conotoxins. The conotoxins can also be used for arresting, protecting or preserving somatic cells. The invention is for the treatment of arrhythmia, urinary incontinence, reperfusion injury, diabetes, retinopathy, neuropathy, nephropathy, acute heart failure, peripheral circulation disturbances, hypertension, angina, cerebral vasospasm accompanying subarachnoid haemorrhage, anxiety disorder, cerebral ischaemia, coronary artery bypass graft (CABG) surgery, ischaemic heart disease, asthma and congestive heart failure. The present sequence is Conus purpurascens (purple cone snail) kappa PVIIA peptide
XX	
SQ	Sequence 27 AA;
	Query Match
	Best Local Similarity 100.0%; Score 120; DB 6; Length 27;
	Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 CXIXNQXCQXQLDCCSXXCNXXKCV 27
Db	1 CXIXNQXCQXQLDCCSXXCNXXKCV 27
RESULT 24	
AAE38346	
ID	AAE38346 standard; peptide; 27 AA.
XX	
AC	AAE38346;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Conus purpurascens kappa-PVIIA analogue peptide, P9Y.
XX	
KW	Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
OS	Conus purpurascens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 4

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XX PF 28-JAN-2003; 2003WO-US002384.
XX PF AAE38358
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 7; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
XX Query Match 100.0%; Score 120; DB 6; Length 27;
XX Best Local Similarity 63.0%; Pred. No. 0.00084;
XX Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CKIPNQKCFQHLDDCCSRKCNRFNKCXV 27
RESULT 26
AAE38358
ID AAE38358 standard; peptide; 27 AA.
AC AAE38358;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX WO2003063782-A2.
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
XX PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
XX CC organ protectants. The invention also relates to a method of arresting,
XX CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX CC related conotoxins. The conotoxins can also be used for arresting,
XX CC protecting or preserving somatic cells. The invention is for the
XX CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX CC peripheral circulation disturbances, hypertension, angina, cerebral
XX CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX CC ischaemic heart disease, asthma and congestive heart failure. The present
XX CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX CC peptide
XX SQ Sequence 27 AA;
XX Query Match 100.0%; Score 120; DB 6; Length 27;
XX Best Local Similarity 63.0%; Pred. No. 0.00084;
XX Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CKIPNQKCFQHLDDCCSRKCNRFNKCXV 27
RESULT 27
AAE38341
ID AAE38341 standard; peptide; 27 AA.
XX AAE38341;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, F9A.
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX Key Location/Qualifiers
XX Modified-site 4 /label= Hyp
XX WO2003063782-A2.
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises

```

xx
cc The invention relates to kappa-PVIIA-related conotoxins and their use as

CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 100.0%; Score 120; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.00084;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXIXNQXCXQLDCCSXXCNXXKCV 27
 DB 1 CRIPNQKCFQALDCCSRKCNRFNKCV 27

RESULT 30
 AAU10212
 ID AAU10212 standard; peptide; 27 AA.
 XX
 AC AAU10212;
 XX
 DT 16-JAN-2002 (first entry)
 XX
 DE Snail Kappa-conotoxin PVIIA analogue S17A.
 XX
 KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; S17A.
 XX
 OS Conus purpurascens.
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 4
 /notes="Hydroxyproline"
 Modified-site 27
 /notes="The C-terminus is either a carboxyl group or an
 amide group"

WO200121648-A1.
 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US025927.
 XX
 PR 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 XX WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 28; 46pp; English.
 XX
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular

CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 117; DB 4; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0015;
 Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXIXNQXCXQLDCCSXXCNXXKCV 27
 DB 1 CRIXNQKCFQHLDDCCARKCNRFNKCV 27

RESULT 31
 AAE38352
 ID AAE38352 standard; peptide; 27 AA.
 XX
 AC AAE38352;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, S17A.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 OS
 FH Key Location/Qualifiers
 FT Modified-site 4
 FT /label= Hyp

WO2003063782-A2.
 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-US002384.
 XX
 PR 29-JAN-2002; 2002US-0352219P.
 XX
 PR (COGN-) COGNETIX INC.
 PR (UTAH) UNIV UTAH RES FOUND.
 PA
 PA Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX
 DR WPI; 2003-679464/64.
 XX
 PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX
 PS Disclosure; Page 7; 32pp; English.
 XX
 CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral,
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 117; DB 6; Length 27;
 Best Local Similarity 59.3%; Pred. No. 0.0015;
 Matches 16; Conservative 11; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNKC 27
 Db 1 CRIPNQKCFQHLDDCCARKCNRFNKC 27

RESULT 32

AAU10217
 ID AAU10217 standard; peptide; 27 AA.

XX AAU10217;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue V27A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; V27A.

OS Conus purpurascens.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an

FT amide group"

FT WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

PR 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

PA Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 PT conotoxin PVIIA peptide.

PS Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 96.7%; Score 116; DB 4; Length 27;

Best Local Similarity 65.4%; Pred. No. 0.0019;

Matches 17; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNKC 26

Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

RESULT 33

AAE38357

ID AAE38357 standard; peptide; 27 AA.

XX AAE38357;

XX 20-NOV-2003 (first entry)

DT Conus purpurascens kappa-PVIIA analogue peptide, V27A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX Conus purpurascens.

XX Key Location/Qualifiers

FT Modified-site 4 /label= Hyp

FT WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 8; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 96.7%; Score 116; DB 6; Length 27;

Best Local Similarity 61.5%; Pred. No. 0.0019;

Matches 16; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXXCNXXNKC 26

Db 1 CRIPNQKCFQHLDDCCSRKCNRFNKC 26

RESULT 34

AAU10214
ID AAU10214 standard; peptide
XX AC AAU10214;
XX DT 16-JAN-07 '1 st at...

XX DE Snail
XX KW Purp
XX KW Carc
XX KW Cc

XX OS C
XX TX C
XX TX C

XX TX C
XX TX C

XX TX C
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XX AC AAU10214;
XX DT 16-JAN-07 '1 st at...

XX DE Snail
XX KW Purp
XX KW Carc
XX KW Cc

XX OS C
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KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

XX Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises

XX use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 6; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
CC peptide

XX Sequence 27 AA;

XX Query Match 95.8%; Score 115; DB 6; Length 27;

XX Best Local Similarity 59.3%; Pred. No. 0.0023;

XX Matches 16; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXKCV 27

DB 1 CRAPNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 37

AAE38354

ID AAE38354 standard; peptide; 27 AA.

XX AC AAE38354;

XX 20-NOV-2003 (first entry)

XX Conus purpurascens kappa-PVIIA analogue peptide, L12A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.

XX

OS Conus purpurascens.

XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;

XX Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises

XX use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 8; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
CC peptide

XX Sequence 27 AA;

XX Query Match 95.8%; Score 115; DB 6; Length 27;

XX Best Local Similarity 59.3%; Pred. No. 0.0023;

XX Matches 16; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXKCV 27

DB 1 CRIPNQKCFQHADDDCCSRKCNRFNKCV 27

RESULT 38

AAU10216

ID AAU10216 standard; peptide; 27 AA.

XX AC AAU10216;

XX 16-JAN-2002 (first entry)

XX Snail Kappa-conotoxin PVIIA analogue Q10A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; Q10A.

OS Conus purpurascens.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
XX 29-MAR-2001.
XX 21-SEP-2000; 2000WO-US025827.
XX 22-SEP-1999; 99US-0155135P.
XX 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX PVIIA) peptide or its analogue, derivative or physiologically active
XX salt. The conotoxins are used for treating disorders associated with
XX radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
XX Sequence 27 AA;
SQ Query Match 95.0%; Score 114; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXCNXXNXCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 39
AAU10210
ID AAU10210 standard; peptide; 27 AA.
XX AAU10210;
XX 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue Q6A.
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
XX cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
XX cerebral ischaemia; ocular ischaemia; asthma; Q6A.
XX Conus purpurascens.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
XX

PD 29-MAR-2001.
XX 21-SEP-2000; 2000WO-US025827.
XX 22-SEP-1999; 99US-0155135P.
XX 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX activating a KATP channel by administering to an individual a kappa-
XX conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX PVIIA) peptide or its analogue, derivative or physiologically active
XX salt. The conotoxins are used for treating disorders associated with
XX radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
XX Sequence 27 AA;
SQ Query Match 95.0%; Score 114; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXCNXXNXCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 40
AAE38356
ID AAE38356 standard; peptide; 27 AA.
XX AAE38356;
XX 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, Q10A.
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX congestive heart failure; neuropathy; nephropathy; CABG.
XX Conus purpurascens.
XX Key Location/Qualifiers
FH Modified-site 4
FT /label= Hyp
XX WO2003063782-A2.
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-US002384.
XX 29-JAN-2002; 2002US-0352219P.
XX (COGN-) COGNETIX INC.
XX

XX	CC	The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
XX	CC	Sequence 27 AA;
XX	CC	Query Match 93.3%; Score 112; DB 4; Length 27;
XX	CC	Best Local Similarity 63.0%; Pred. No. 0.0041;
XX	CC	Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
QY	1	CXIXNQXCXQXLLDCCSXXCNXXNXCXV 27
		: : : :
Db	1	CRIXNQCFQHLDDACCSKCNRFNKCXV 27
RESULT 44		
AAU10219		ID AAU10219 standard; peptide; 27 AA.
ID	AAU10219	standard; peptide; 27 AA.
XX	AC	AAU10219;
XX	DT	16-JAN-2002 (first entry)
XX	XX	Snail Kappa-conotoxin PVIIA analogue NSA.
DE	XX	Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
XX	KW	cardioactive; antiasthmatic; KATP channel activation; cerebral ischaemia; ocular ischaemia; asthma; NSA.
KW	KW	cerebral ischaemia; ocular ischaemia; asthma; NSA.
XX	OS	Conus purpurascens.
OS	OS	Synthetic.
XX	XX	Key Location/Qualifiers
FT	FT	Modified-site 4
FT	FT	/note= "Hydroxyproline"
FT	FT	Modified-site 27
FT	FT	/note= "The C-terminus is either a carboxyl group or an amide group"
XX	XX	WO200121648-A1.
PN	XX	29-MAR-2001.
PD	XX	21-SEP-2000; 2000WO-US025827.
XX	XX	22-SEP-1999; 99US-0155135P.
PR	XX	20-JUL-2000; 2000US-0219438P.
PR	XX	(COGN-) COGNETIX INC.
PA	XX	Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT; Jones RR;
PI	XX	WPI; 2001-648090/74.
PI	XX	Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
DR	XX	Claim 1; Page 28; 46pp; English.
XX	XX	The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt.

CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
XX Sequence 27 AA;
SQ
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CXIXNQXCQXLDCCSXCNXXNKCVCV 27
Db 1 CRIXAQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 45
AAU10215
ID AAU10215 standard; peptide; 27 AA.
XX AC AAU10215;
XX AC
XX 16-JAN-2002 (first entry)
XX DE
XX Snail Kappa-conotoxin PVIIA analogue D13A.
XX DE
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; D13A.
XX KW
XX Conus purpurascens.
OS Synthetic.
XX OS
XX Key Location/Qualifiers
FT Modified-site 4
FT Modified-site 27 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
XX PN
XX 29-MAR-2001.
XX PD
XX 21-SEP-2000; 2000WO-US025827.
XX PF
XX 22-SEP-1999; 99US-0155135P.
XX PR
XX 20-JUL-2000; 2000US-0219438P.
XX PR
XX (COGN-) COGNETIX INC.
XX PA
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX PI Jones RR;
XX PT
XX WPI; 2001-648090/74.
XX DR
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX PT activating a KATP channel by administering to an individual a kappa-
XX PT conotoxin PVIIA peptide.
XX DR
XX Claim 1; Page 28; 46pp; English.
XX PS
XX The invention relates to treating disorders associated with radical
XX CC depolarisation of excitable membrane by activating a KATP channel
XX CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX CC PVIIA) peptide or its analogue, derivative or physiologically active
XX CC salt. The conotoxins are used for treating disorders associated with
XX CC radical depolarisation of excitable membrane by activating a KATP
XX CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX CC analogue of the invention

XX SQ Sequence 27 AA;
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CXIXNQXCQXLDCCSXCNXXNKCVCV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 46
AAU10211
ID AAU10211 standard; peptide; 27 AA.
XX AC AAU10211;
XX AC
XX 16-JAN-2002 (first entry)
XX DT
XX Snail Kappa-conotoxin PVIIA analogue N21A.
XX DE
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; N21A.
XX KW
XX Conus purpurascens.
OS Synthetic.
XX OS
XX Key Location/Qualifiers
FT Modified-site 4
FT Modified-site 27 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
XX WO200121648-A1.
XX PN
XX 29-MAR-2001.
XX PD
XX 21-SEP-2000; 2000WO-US025827.
XX PF
XX 22-SEP-1999; 99US-0155135P.
XX PR
XX 20-JUL-2000; 2000US-0219438P.
XX PR
XX (COGN-) COGNETIX INC.
XX PA
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX PI Jones RR;
XX PT
XX WPI; 2001-648090/74.
XX DR
XX Treating disorders associated with radical depolarization of excitable
XX membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
XX PT activating a KATP channel by administering to an individual a kappa-
XX PT conotoxin PVIIA peptide.
XX DR
XX Claim 1; Page 28; 46pp; English.
XX PS
XX The invention relates to treating disorders associated with radical
XX CC depolarisation of excitable membrane by activating a KATP channel
XX CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX CC PVIIA) peptide or its analogue, derivative or physiologically active
XX CC salt. The conotoxins are used for treating disorders associated with
XX CC radical depolarisation of excitable membrane by activating a KATP
XX CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX CC analogue of the invention
XX SQ Sequence 27 AA;
Query Match 93.3%; Score 112; DB 4; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.0041;

RESULT 49
AAE38355
ID AAE38355 standard; peptide; 27 AA.

DE	Conus purpurascens kappa-PVIIA analogue peptide, D14A.
KW	Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW	ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW	organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW	reintopathy; coronary artery bypass graft surgery; acute heart failure;
KW	congestive heart failure; neuropathy; nephropathy; CABG.
XX	
OS	Conus purpurascens.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 4 /label= Hyp
XX	
PN	WO2003063782-A2.
XX	
PD	07-AUG-2003.
XX	
PF	28-JAN-2003; 2003WO-US002384.
XX	
PR	29-JAN-2002; 2002US-0352219P.
XX	
PA	(COGN-) COGNETIX INC.
FA	(UTAH) UNIV UTAH RES FOUND.
XX	
PI	Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI	Oliviera BM;
XX	
XX	WPI: 2003-679464/64.
DR	
PT	Protection and preservation of an organ e.g. heart of a mammal comprises
PT	use of a compound binding to kappa-PVIIA-binding site.
XX	
PS	Disclosure; Page 7; 32pp; English.
XX	
CC	The invention relates to kappa-PVIIA-related conotoxins and their use as
CC	organ protectants. The invention also relates to a method of arresting,
CC	protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC	related conotoxins. The conotoxins can also be used for arresting,
CC	protecting or preserving somatic cells. The invention is for the
CC	treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC	diabetes, reintopathy, neuropathy, nephropathy, acute heart failure,
CC	peripheral circulation disturbances, hypertension, angina, cerebral
CC	vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC	cerebral ischaemia, coronary artery bypass graft (CABG) surgery.
CC	ischaemic heart disease, asthma and congestive heart failure. The present
CC	sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
CC	peptide
XX	
SQ	Sequence 27 AA;
Query Match	93.3%; Score 112; DB 6; Length 27;
Best Local Similarity	59.3%; Pred. No. 0.0041;
Matches	16; Conservative 10; Mismatches 1; Indels 0; Gaps 0
Qy	1 CXINXOXCXOXLDPCSXGXCNXNKCVCV 27
Db	1 CRIPNQCFQLDACCRRKCNRFNKVCV 27 .
RESULT 51	
AAE38359	
ID	AAE38359 standard; peptide; 27 AA.
XX	
AC	AAE38359;
XX	
DT	20-NOV-2003 (first entry)
XX	
DE	Conus purpurascens kappa-PVIIA analogue peptide, N5A.
XX	
KW	Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW	ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW	organ protectant; arrhythmia; reperfusion injury; hypertension; angina;

KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.

Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT

PN WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 FT use of a compound binding to kappa-PVIA-binding site.
 XX

PS Disclosure; Page 8; 32pp; English.

XX The invention relates to kappa-PVIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIA analogue
 XX peptide

XX Sequence 27 AA;

Query Match 93.3%; Score 112; DB 6; Length 27;
 Best Local Similarity 63.0%; Pred. No. 0.0041;

Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNKC 27

Db 1 CRXAQKCFQHLDDCCSRKCNRFNKC 27

RESULT 52

AAR39628

ID AAR39628 standard; peptide; 26 AA.

XX AC AAR39628;

XX 25-MAR-2003 (revised)

DT 20-DEC-1993 (first entry)

XX SNX-202.

XX Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;

KW calcium channel; neurone; contraction; guinea pig; ileum; MWIIA;

KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;

KW narcotics.

XX Synthetic.

OS

XX

Key Location/Qualifiers
 FH Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26
 FT Modified-site 26
 FT /note= "Amidated C-terminal"

XX WO9313128-A1.

XX 08-JUL-1993.

XX 30-DEC-1992; 92WO-US011349.

XX 30-DEC-1991; 91US-00814759.

XX (NEUR-) NEUREX CORP.

XX Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;

XX WPI; 1993-227270/28.

XX Use of omega-cono-peptide(s) which selectively inhibit voltage-gated

XX calcium channels - to induce analgesia, enhance opiate analgesics, treat

XX pain etc.

XX Claim 1; Fig 2; 90pp; English.

XX The sequences given in AAR39608-30 are omega conopeptides (OCTs) and

XX derivatives of these, which may be used to produce analgesia in a mammal.

XX These OCTs inhibit voltage-gated calcium channels selectively in neuronal

XX tissue. This is shown by the peptides ability to stimulate contraction in

XX guinea pig ileum and to bind to OCT MWIIA binding sites present in

XX neuronal tissue. OCTs are components of peptide toxins derived from

XX marine snails of the genus Conus, and act as calcium channel blockers.

XX These OCTs may be used to replace opiods in the treatment of chronic pain

XX or to reduce the opiod dosage required. This helps to reduce dependence

XX on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct

XX PN field.)

XX Sequence 26 AA;

XX Query Match 67.5%; Score 81; DB 2; Length 26;

XX Best Local Similarity 34.6%; Pred. No. 2;

XX Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNXC 26

Db 1 CKLKGQSCSRMLYDCCSGSGRSGKC 26

RESULT 53

AAR37774

ID AAR37774 standard; peptide; 26 AA.

XX AC AAR37774;

XX 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX SNX-202.

XX Ischaemia; neuronal; omega-conotoxin; OCT; MWIIA; MVIIIC; MWIID; MWIIB;

KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;

KW antihistamine; blood pressure; N-type voltage-gated Ca currents;

KW N-channel mediated neurotransmitter release.

XX Synthetic.

OS

XX

XX Key Location/Qualifiers

FT Disulfide-bond 1. .16

FT Disulfide-bond 8. .20

FT Disulfide-bond 15. .26

XX

PN W09310145-A1.
 XX 27-MAY-1993.
 XX 12-NOV-1992; 92WO-US009766.
 XX 12-NOV-1991; 91US-00789913.
 PR 17-JUL-1992; 92US-00916478.
 XX (NEUR-) NEUREX CORP.
 XX Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
 PI Yamashiro DH;
 PI WPI; 1993-182487/22.
 DR Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
 PT bind specifically to omega-conotoxin MWIIA binding sites.
 XX Disclosure; Fig 2; 103pp; English.
 CC The C-terminal is amidated. Ischaemia-related neuronal damage in mammals
 CC is reduced by admin., 4-24 hr after onset of ischaemia, of a cpd. (I)
 CC which binds selectively to an omega-conotoxin (OCT) MWIIA site in
 CC neuronal tissue. (I) has selectivity at least 100 expressed as ratio of
 CC binding affinity for the MWIIA site to that for the MWIIC site. (I) is
 CC one of the OCTs MWIIA, MWIIB, GVIA, GVIIA or RVIA or it is the cpd. SNX-
 CC 207. (I) is esp. used to reduce neuronal damage caused by stroke. By
 CC delaying admin. for some time (compare US051403 where cpds. are given
 CC within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage
 CC is achieved. (I) is admin. e.g. by intracerebroventricular (ICV)
 CC injection at 0.1-20 microg/kg, but can also be given i.v. (opt. after
 CC treatment with antihistamines to minimise redn. in blood pressure caused
 CC by (I)). (I) is also at least as effective as the specified conotoxins
 CC for (1) selective inhibition of N-type voltage-gated Ca currents in
 CC neuronal tissue and (2) selective inhibition of N-channel mediated
 CC neurotransmitter release in neuronal tissue. Primary sequences of omega-
 CC conopeptides are given in AAR37752-62. Several analog omega-conopeptides
 CC are given in AAR37763-76. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 26 AA;
 Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;
 Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXQXLDCCSCXXCNXXNC 26
 DB 1 CLKUGQSCRLMYDCCSGCGRGKC 26
 RESULT 54
 AAW19570
 ID AAW19570 standard; peptide; 26 AA.
 AC AAW19570;
 XX 14-OCT-1997 (first entry)
 DT SNX-202, omega conopeptide derivative used for pain relief.
 DE Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
 XX N-type voltage-sensitive calcium channel; block; Conus.
 KW Synthetic.
 OS Key Location/Qualifiers
 FT Modified-site 26
 FT /note= "amidated"
 XX W09701351-A1.
 XX 16-JAN-1997.
 XX 26-JUN-1996; 96WO-US011041.
 XX 27-JUN-1995; 95US-00496847.
 PR 08-MAR-1996; 96US-00613400.
 XX (NEUR-) NEUREX CORP.
 XX Amstutz GA, Bowersox SS, Gohl K, Adriaenssens PI, Kristipati R;
 PI Gadbois T, Pettus MR, Luther RR;
 XX WPI; 1997-100012/09.
 DR Stable omega conopeptide compositions - for producing analgesia and for
 PT inhibiting progression of neuropathic pain disorders.
 XX Disclosure; Fig 4; 47pp; English.
 CC AAW19555-W19572 are omega conopeptides (OCs) derived from natural
 CC peptides from Conus sp. (cone snails). The peptides and their analogues
 CC are used as analgesics acting by blocking N-type voltage-sensitive
 CC calcium channels. The OCs can be used to treat neuropathic pain as a
 CC result of e.g. insult to the spinal cord or peripheral nerves, cancer,
 CC bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes
 CC zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
 CC hyperalgesia. The OCs are preferably administered in a medicament via an
 CC epidural route in a continuous infusion or sustained release formulation.
 CC The OCs can provide pain relief when administered epidurally in the
 CC absence of a permeation enhancer, at doses that are comparable to
 CC effective analgesic doses using intrathecal administration. OC
 CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
 CC They also confer stability to solutions containing them for prolonged
 CC treatment methods and long-term storage
 XX SQ Sequence 26 AA;
 Query Match 67.5%; Score 81; DB 2; Length 26;
 Best Local Similarity 34.6%; Pred. No. 2;
 Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXQXLDCCSCXXCNXXNC 26
 DB 1 CLKUGQSCRLMYDCCSGCGRGKC 26
 RESULT 55
 AAW12985
 ID AAW12985 standard; peptide; 26 AA.
 XX AAW12985;
 XX 25-MAR-2003 (revised)
 DT 22-APR-1997 (first entry)
 XX Omega conopeptide SNX-202.
 DE Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
 XX neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
 KW acute dystonic reactions; inflammation; epilepsy.
 OS Synthetic.
 XX US5587454-A.
 PN 24-DEC-1996.
 PD 15-APR-1993; 93US-00049794.
 XX 30-DEC-1991; 91US-00814759.
 PR 30-DEC-1992; 92WO-US011349.
 XX (NEUR-) NEUREX CORP.
 XX

PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
XX WPI; 1997-064830/06.
XX Omega cono:peptide(s) - useful as analgesics, esp. for treating
PT neuropathic pain.
XX
PS Disclosure; Col 51-52; 58pp; English.
XX
XX The present peptide is an omega conopeptide, useful as an analgesic,
CC especially for treating neuropathic pain. The peptide, which can be
CC prepared by solid phase synthesis, can also be used to inhibit neuronal
CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
CC reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 26 AA;
Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 2;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 CXIXNQXQXQLDDCCSXCNXXNC 26
DB 1 CKLKGQSCSRLMYDCCSGCGRSKGC 26
RESULT 56
AAW72625
ID AAW72625 standard; peptide; 26 AA.
XX
AC AAW72625;
XX
DT 27-AUG-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Conus genus analogue omega-conopeptide SNX-202.
XX
XX Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
XX nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
KW rheumatoid arthritis; epilepsy.
XX
OS Conus.
XX
XX US5824645-A.
XX
XX 20-OCT-1998.
XX
XX 01-NOV-1996; 96US-00742774.
XX
XX 30-DEC-1991; 91US-00814759.
XX 15-APR-1993; 93US-00049794.
XX 03-JUL-1996; 96US-00675354.
XX
XX (NEUR-) NEUREX CORP.
XX
XX Miljanich GP, Valentino KL, Gohil KC, Justice A, Singh T;
XX WPI; 1998-582596/49.
XX
XX Treatment of inflammation, comprises administration of omega-conopeptide
PT - effective to block voltage-gated calcium channels, bind with high
PT affinity to omega-conopeptide binding site, and inhibit neuro-transmitter
PT release.
XX
PS Disclosure; Fig 2; 58pp; English.
XX
XX A method has been developed for the treatment of inflammation in a
CC subject. The method comprises administration of an omega-conopeptide
CC effective to: (i) block voltage-gated calcium channels; (ii) bind with
CC high affinity to an omega-conopeptide binding site; and (iii) inhibit
CC neurotransmitter release from nervous tissue. The method is used to treat

CC inflammation and associated pain. The treatment can also be used to
CC produce analgesia (especially in subjects experiencing neuropathic pain);
CC and to treat schizophrenia, tardive dyskinesia and acute dystonic
CC reactions, rheumatoid arthritis, and epilepsy. The present sequence
CC represents an analogue omega-conopeptide. Omega-conopeptides are
CC components of peptide toxins produced by marine snails of the genus
CC Conus, and which act as calcium channel blockers. (Updated on 27-AUG-2003
CC to correct OS field.)
XX
SQ Sequence 26 AA;
Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 2;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
QY 1 CXIXNQXQXQLDDCCSXCNXXNC 26
DB 1 CKLKGQSCSRLMYDCCSGCGRSKGC 26
RESULT 57
AAW95584
ID AAW95584 standard; protein; 26 AA.
XX
AC AAW95584;
XX
DT 29-MAR-1999 (first entry)
XX
DE Analog omega-conopeptide SNX-202.
XX
KW Omega-conopeptide; peptide toxin; snail; calcium channel blocker;
KW analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
XX
XX Synthetic.
OS Conus sp.
XX
XX Key Location/Qualifiers
FH Modified-site 25 /note= "C-terminal amide"
FT
XX
XX US5859186-A.
XX
XX 12-JAN-1999.
XX
XX 03-JUL-1996; 96US-00675354.
XX
XX 30-DEC-1991; 91US-00814759.
XX 15-APR-1993; 93US-00049794.
XX
XX (NEUR-) NEUREX CORP.
XX
XX Miljanich GP, Gohil KC, Valentino KL, Justice A, Singh T;
XX WPI; 1999-120002/10.
XX
XX Production of analgesia in mammal - by administration of omega cono-
PT peptide(s).
XX
XX Disclosure; Fig 2A-B; 59pp; English.
XX
XX Sequences AAW95574-589 represent sequences of analog omega-conopeptides.
CC Omega-conopeptides are components of peptide toxins produced by marine
CC snails of the genus Conus, and which act as calcium channel blockers. The
CC invention relates to a method of producing analgesia in a mammal that
CC comprises administering an omega conopeptide having activities in (a)
CC inhibiting electrically stimulated contraction of guinea pig ileum and
CC (b) selectively binding to omega conopeptide MVIIA binding sites in
CC neuronal tissue, where these activities are within the ranges of those of
CC omega-conotoxins MVIIA and TVIA. The method is used for treating chronic
CC pain, especially neuropathic pain
XX
XX Sequence 26 AA;
SQ

QY 1 CXIXNQXCXOXLDCCSXCNXXNC 26
 Db 1 CKLKQSCSRMLYDCCSGSGRSGKC 26

RESULT 60

AAB19462
 ID AAB19462 standard; peptide; 26 AA.

AC AAB19462;

DT 06-MAR-2001 (first entry)

DE Sequence of an omega-conopeptide analogue designated SNX-202.

KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.

OS Synthetic.

OS Conus sp.

FH Key Location/Qualifiers

FT Modified-site 26

FT /note= "amidated residue"

PN US6136786-A.

PD 24-OCT-2000.

PF 09-SEP-1999; 99US-00392979.

PR 30-DEC-1991; 91US-00814759.

PR 15-APR-1993; 93US-00049794.

PR 23-JUN-1993; 93US-00081863.

PR 03-JUL-1996; 96US-00675354.

PR 01-NOV-1996; 96US-00742774.

PR 21-AUG-1998; 98US-00138439.

PR 23-APR-1999; 99US-00298017.

PA (ELAN-) ELAN PHARM INC.

PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;

DR WPI; 2001-030946/04.

PT Enhancing analgesia produced by opiates by administering an omega-
 PT conopeptide that inhibits electrically stimulated contraction of guinea
 PT pig ileum and binds to omega-conopeptide MWIIA binding sites in neuronal
 PT tissues.

PS Disclosure; Col 51-52; 58pp; English.

CC The present sequence represents an omega-conopeptide analogue. Omega-
 CC conopeptides are components of peptide toxins which act as voltage-gated
 CC calcium channel inhibitors. The peptides are used to enhance the
 CC analgesic effect produced by an opiate in a mammalian subject. The method
 CC comprises administering to the subject an omega-conopeptide which is able
 CC to inhibit electrically stimulated contraction of the guinea pig ileum
 CC and bind to omega-conopeptide MWIIA binding sites present in neuronal
 CC tissue. Omega-conopeptides are useful for enhancing the analgesic effect
 CC produced by an opiate. Omega-conopeptides may also be used in the
 CC treatment of pain, in reducing neuronal damage related to an ischemic
 CC condition in mammals, and in treating schizophrenia, tardive dyskinesia
 CC and acute dystonic reactions, inflammation and epilepsy

XX Sequence 26 AA;

Query Match " 67.5%; Score 81; DB 4; Length 26;

Best Local Similarity 34.6%; Pred. No. 2;

Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXIXNQXCXOXLDCCSXCNXXNC 26
 Db 1 CKLKQSCSRMLYDCCSGSGRSGKC 26

RESULT 61

ABB96887
 ID ABB96887 standard; peptide; 26 AA.

XX ABB96887;

DT 12-JUL-2002 (first entry)

DE Omega-conopeptide S6.2 toxin sequence.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus striatus.

PN WO200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

PR 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;

PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.

PS Claim 1(a); Page 72; 195pp; English.

CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences

XX Sequence 26 AA;

Query Match 67.5%; Score 81; DB 5; Length 26;

Qv 1 CXIXNOXCXQXLDCCSXXCNXXXNC 26

Matches	9;	Conservative	12;	Mismatches	5;	Indels	0;	Gaps	0;
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```

1 CXIXNQXCQXLDDCCSXXCNXXNC 26
|::|::|::|::|::|::|::|::|::|
1 CKLKGQSCRKTSYDCCSGSCGRSGKC 26

```

[illegible]

xx. PT Selecting a compound for producing analgesia involves measuring activity

PT of test compound in blocking voltage-gated calcium channels, binding to
 XX omega conopeptide binding site and inhibiting norepinephrine release.
 PS Example 4; Fig 1; 58pp; English.
 CC The present sequence is an omega-conopeptide from marine snails of the
 CC genus Conus. Omega-conopeptides are components of peptide toxins produced
 CC by the cone snails, and which act as calcium channel blockers. Natural
 CC omega-conopeptides and their derivatives may be useful for producing
 CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega
 CC -conopeptide binding sites, which are present mainly in neuronal tissue,
 CC and inhibit norepinephrine release from nervous tissue. Conopeptides such
 CC as MWIIA and TVIA are effective as therapeutic agents for treating
 CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
 CC dystonic reactions, inflammation and epilepsy
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 3; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSXCNXNXC 26
 DB 1 CLKKGQSCRKTSYDCCSGSGCRSGKC 26
 RESULT 71
 AAB92221
 ID AAB92221 standard; peptide; 26 AA.
 AC AAB92221;
 XX
 XX 22-JUN-2001 (first entry)
 DE Toxin peptide SEQ ID NO:1397.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 KW
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO20069900-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000WO-US013576.
 XX
 XX 17-MAY-1999; 99US-0134406P.
 XX 10-SEP-1999; 99US-0153406P.
 XX 15-OCT-1999; 99US-0159783P.
 XX
 XX (CONJ-) CONJUCHEM INC.
 XX
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
 XX WPI; 2001-112059/12.
 XX
 XX Modifying and attaching therapeutic peptides to albumin prevents
 XX peptidase degradation, useful for increasing length of in vivo activity.
 XX
 XX Disclosure; Page 653-654; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in

CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 26 AA;
 Query Match 64.2%; Score 77; DB 4; Length 26;
 Best Local Similarity 34.6%; Pred. No. 4.4;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXOXLDCCSXCNXNXC 26
 DB 1 CLKKGQSCRKTSYDCCSGSGCRSGKC 26
 RESULT 72
 AAB19449
 ID AAB19449 standard; peptide; 26 AA.
 XX
 XX AAB19449;
 AC
 XX
 XX 06-MAR-2001 (first entry)
 DT
 XX
 XX Primary sequence of a natural omega-conopeptide SVIB/SNX-183.
 DE
 XX
 KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.
 KW
 XX Conus sp.
 OS
 XX
 XX Key Location/Qualifiers
 XX Disulfide-bond 1..15
 XX Disulfide-bond 8..19
 XX Disulfide-bond 15..26
 XX Modified-site 26
 XX /note= "amidated C-terminal"
 XX
 XX US6136786-A.
 XX
 XX 24-OCT-2000.
 XX
 XX 09-SEP-1999; 99US-00392979.
 XX
 XX 30-DEC-1991; 91US-00814759.
 XX 15-APR-1993; 93US-00049794.
 XX 23-JUN-1993; 93US-00081863.
 XX 03-JUL-1996; 96US-00675354.
 XX 01-NOV-1996; 96US-00742774.
 XX 21-AUG-1998; 98US-00138439.
 XX 23-APR-1999; 99US-00298017.
 XX
 XX (ELAN-) ELAN PHARM INC.
 XX
 XX Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX WPI; 2001-030946/04.
 XX
 XX Enhancing analgesia produced by opiates by administering an omega-
 XX conopeptide that inhibits electrically stimulated contraction of guinea
 XX pig ilium and binds to omega-conopeptide MWIIA binding sites in neuronal
 XX tissues.
 XX
 XX Disclosure; Fig 1; 58pp; English.
 PS
 XX The present sequence represents an omega-conopeptide. Omega-conopeptides

Qy	1	CXIXNQXCXQXLD	CCSXXCNXXNC	26
		:::	:::	:
		:::	:::	:
Db	1	CKLKGQSCRKTSYD	CCSGSGRSGKC	26

CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB9698-A3B96806 represent omega-conopeptide
 CC generic toxin sequences
 XX
 SQ Sequence 26 AA; .

Query Match 58.3%; Score 70; DB 5; Length 26;
 Best Local Similarity 34.6%; Pred. No. 18;
 Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNQXQXLDCCSXXCNXXNC 26
 Db 1 CKLKGQSCRKTSXCCSGSGCRGKC 26

RESULT 77
 AAR39616
 ID AAR39616 standard; peptide; 26 AA.
 XX
 AC AAR39616;

DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)

DE MVIIC/SNX230.

KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MVIIC;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.

OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26

PN WO9313128-A1.

PD 08-JUL-1993.

PF 30-DEC-1992; 92WO-US011349.

PR 30-DEC-1991; 91US-00814759.

PA (NEUR-) NEUREX CORP.

PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 DR WPI; 1993-227270/28.

PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.

PS Claim 1; Fig 1; 90pp; English.

CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MVIIC binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 2; Length 26;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXQXLDCCSXXCNXXNC 26
 Db 1 CKGKAPCRKTYDCCSGSGCRGKC 26

RESULT 78

AAR39617
 ID AAR39617 standard; peptide; 26 AA.

XX
 AC AAR39617;

DT 25-MAR-2003 (revised)

DT 20-DEC-1993 (first entry)

DE SNX231.

KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; MVIIC;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.

OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Modified-site 7. /note="4Hyp"
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26

PN WO9313128-A1.

PD 08-JUL-1993.

PF 30-DEC-1992; 92WO-US011349.

PR 30-DEC-1991; 91US-00814759.

PA (NEUR-) NEUREX CORP.

PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 DR WPI; 1993-227270/28.

PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.

PS Claim 1; Fig 1; 90pp; English.

CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT MVIIC binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 2; Length 26;
 Best Local Similarity 30.8%; Pred. No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY		1	CXIXNQXCXOXLDCCSXXCNXXNYC 26
		:	: ::: :: ::
DB		1	CRKGAGPCRKTMYDCCSGCGRRGKC 26
RESULT	79		
AAR37762		ID	AAR37762 standard; peptide; 26 AA.
XX		AC	AAR37762;
XX		DT	(revised)
DT		08-SEP-1993	(first entry)
XX		SNX-231.	
XX			
KW			Ichaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MWIID; MVIIB; MVIIB;
KW			GVIIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
KW			antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW			N-channel mediated neurotransmitter release.
XX			
OS			Synthetic.
XX			
FH		Key	Location/Qualifiers
FT		Disulfide-bond	1..16
FT		Modified-site	7
FT		/note=	"hydroxyproline"
FT		Disulfide-bond	8..20
FT		Disulfide-bond	15..26
XX			
PX		WO9310145-A1.	
XX			
PD		27-MAY-1993.	
XX			
PF		12-NOV-1992;	92WO-US009766.
XX			
PR		12-NOV-1991;	91US-00789913.
PR		17-JUL-1992;	92US-00916478.
XX			
PA		(NEUR-) NEUREX CORP.	
XX			
PI		Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;	
PI		Yamashiro DH;	
PS		WPI; 1993-182487/22.	
DR			
XX			
PT		Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that	
PT		bind specifically to omega-conotoxin MVIIA binding sites.	
XX			
PS		Disclosure; Fig 1; 103pp; English.	
XX			
CC		Ichaemia-related neuronal damage in mammals is reduced by admin., 4-24	
CC		hr after onset of ischaemia, of a cpd. (I) which binds selectively to an	
CC		omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity	
CC		at least 100 expressed as ratio of binding affinity for the MVIIA site to	
CC		that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA	
CC		or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal	
CC		damage caused by stroke. By delaying admin. for some time (compare	
CC		US0501403 where cpds. are given within 1 hr of the onset of ischaemia) a	
CC		greater redn. in neuronal damage is achieved. (I) is admin. e.g. by	
CC		intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also	
CC		be given i.v. (opt. after treatment with antihistamines to minimise redn.	
CC		in blood pressure caused by (I)). (I) is also at least as effective as	
CC		the specified conotoxins for (1) selective inhibition of N-type voltage-	
CC		-gated Ca currents in neuronal tissue and (2) selective inhibition of N-	
CC		channel mediated neurotransmitter release in neuronal tissue. Primary	
CC		sequences of omega-conopeptides are given in AAR37752-62. Several analog	
CC		omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to	
CC		correct PN field.)	
XX			
SQ		Sequence 26 AA;	

```

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXNXC 25
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMVDCSGSGRGRKC 25

RESULT 81
AAW19552
ID AAW19552 standard; peptide; 26 AA.
XX
AC AAW19552;
XX
DT 27-AUG-2003 (revised)
DT 13-OCT-1997 (first entry)
XX
DE Natural omega-conopeptide MWIIC/SNX-230 used for pain relief.
XX
KW Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
KW N-type voltage-sensitive calcium channel; block; Conus.
XX
OS Conus.
XX
PN WO9701351-A1.
XX
PD 16-JAN-1997.
XX
PF 26-JUN-1996; 96WO-US011041.
XX
PR 27-JUN-1995; 95US-00496847.
PR 08-MAR-1996; 96US-00613400.
XX
PA (NEUR-) NEUREX CORP.
XX
PI Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
PI Gadbois T, Pettus MR, Luther RR;
XX
DR WPI; 1997-100012/09.
XX
PT Stable omega conopeptide compositions - for producing analgesia and for
PT inhibiting progression of neuropathic pain disorders.
XX
PS Disclosure; Fig 2; 47pp; English.
XX
CC AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated
CC from Conus sp. (cone snails). The peptides and their analogues are used
CC as analgesics acting by blocking N-type voltage-sensitive calcium
CC channels. The OCs can be used to treat neuropathic pain as a result of
CC e.g. insult to the spinal cord or peripheral nerves, cancer, bone
CC degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster
CC neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
CC hyperalgesia. The OCs are preferably administered in a medicament via an
CC epidural route in a continuous infusion or sustained release formulation.
CC The OCs can provide pain relief when administered epidurally in the
CC absence of a permeation enhancer, at doses that are comparable to
CC effective analgesic doses using intrathecal administration. OC
CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
CC They also confer stability to solutions containing them for prolonged
CC treatment methods and long-term storage. (Updated on 27-AUG-2003 to
CC correct OS field.)
XX
SQ Sequence 26 AA;

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXNXC 26
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMVDCSGSGRGRKC 26

RESULT 82
AAW12987
ID AAW12987 standard; peptide; 26 AA.
XX
AC AAW12987;
XX
DT 25-MAR-2003 (revised)
DT 22-APR-1997 (first entry)
XX
DE Omega conopeptide SNX-231.
XX
KW Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
KW neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
KW acute dystonic reactions; inflammation; epilepsy.
XX
OS Synthetic.
XX
FH Key
FH Modified-site 7
FH Location/Qualifiers
FT FT /label= Hyp
XX
PN US5587454-A.
XX
PD 24-DEC-1996.
XX
PF 15-APR-1993; 93US-00049794.
XX
PR 30-DEC-1991; 91US-00814759.
PR 30-DEC-1992; 92WO-US011349.
XX
PA (NEUR-) NEUREX CORP.
XX
PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
PI WPI; 1997-064830/06.
XX
DR Omega conopeptide(s) - useful as analgesics, esp. for treating
DR neuropathic pain.
XX
PT Disclosure; Col 53-54; 58pp; English.
XX
CC The present peptide is an omega conopeptide, useful as an analgesic,
CC especially for treating neuropathic pain. The peptide, which can be
CC prepared by solid phase synthesis, can also be used to inhibit neuronal
CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
CC reactions, inflammation and epilepsy. In a rat paw formalin test, the
CC peptide had an ED50 of greater than 1.0 microg in phase 1, and greater
CC than 1.0 microg in phase 2 (by intrathecal administration). (Updated on
CC 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 26 AA;

Query Match          57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 22;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXNXC 26
   | : : : : : | | | : : : | : : |
DB 1 CKGKAPCRKTMVDCSGSGRGRKC 26

RESULT 83
AAW72614
ID AAW72614 standard; peptide; 26 AA.
XX
AC AAW72614;
XX
DT 27-AUG-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
DE Conus genus natural omega-conopeptide MWIIC/SNX-230.

```



```

FT Modified-site /note= "4-Hydroxyproline"
FT 26
FT /note= "C-terminal amide"
XX
PN US5859186-A.
XX
PD 12-JAN-1999.
XX
PF 03-JUL-1996; 96US-00675354.
XX
PR 30-DEC-1991; 91US-00814759.
PR 15-APR-1993; 93US-00049794.
XX
XX (NEUR-) NEUREX CORP.
XX
PI Miljanich GP, Gohil KC, Valentino KL, Justice A, Singh T;
XX WPI; 1999-120002/10.
XX
PT Production of analgesia in mammal - by administration of omega cono-
PT peptide(s).
XX
PS Disclosure; Fig 1B; 59pp; English.
XX
CC Sequences AAW95564-573 represent primary sequences of natural omega-
CC conopeptides. Omega-conopeptides are components of peptide toxins
CC produced by marine snails of the genus Conus, and which act as calcium
CC channel blockers. The invention relates to a method of producing
CC analgesia in a mammal that comprises administering an omega conopeptide
CC having activities in (a) inhibiting electrically stimulated contraction
CC of guinea pig ileum and (b) selectively binding to omega conopeptide
CC MVIIA binding sites in neuronal tissue, where these activities are within
CC the ranges of those of omega-conotoxins MVIIA and TVIA. The method is
CC used for treating chronic pain, especially neuropathic pain
XX
XX SQ Sequence 26 AA;
XX
Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
QY 1 CXINQXCXQXLDCCSCXCNXKNC 26
| : : : : : |
Db 1 CKGKGAFCRKTMYDCCSGCGRRGKC 26
| : : : : : |

RESULT 87
AAW5573
ID AAW95573 standard; protein; 26 AA.
XX
AC AAW95573;
XX
DT 29-MAR-1999 (first entry)
XX
DE Omega-conopeptide SNX-230.
XX
KW Omega-conopeptide; peptide toxin; snail; calcium channel blocker;
KW analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
XX
OS Synthetic.
OS Conus sp.
XX
FH Key Location/Qualifiers
FT Modified-site 26
FT /note= "C-terminal amide"
XX
PN US5859186-A.
XX
PD 12-JAN-1999.
XX
PF 03-JUL-1996; 96US-00675354.
XX
PR 30-DEC-1991; 91US-00814759.
XX
XX WPI; 1999-120002/10.
XX
PT Production of analgesia in mammal - by administration of omega cono-
PT peptide(s).
XX
PS Disclosure; Fig 1B; 59pp; English.
XX
CC Sequences AAW95564-573 represent primary sequences of natural omega-
CC conopeptides. Omega-conopeptides are components of peptide toxins
CC produced by marine snails of the genus Conus, and which act as calcium
CC channel blockers. The invention relates to a method of producing
CC analgesia in a mammal that comprises administering an omega conopeptide
CC having activities in (a) inhibiting electrically stimulated contraction
CC of guinea pig ileum and (b) selectively binding to omega conopeptide
CC MVIIA binding sites in neuronal tissue, where these activities are within
CC the ranges of those of omega-conotoxins MVIIA and TVIA. The method is
CC used for treating chronic pain, especially neuropathic pain
XX
XX SQ Sequence 26 AA;
XX
Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
QY 1 CXINQXCXQXLDCCSCXCNXKNC 26
| : : : : : |
Db 1 CKGKGAFCRKTMYDCCSGCGRRGKC 26
| : : : : : |

RESULT 87
AAW56482
ID AAY56482 standard; peptide; 26 AA.
XX
AC AAY56482;
XX
DT 16-FEB-2000 (first entry)
XX
DE Natural omega conopeptide SNX-231.
XX
KW Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin;
KW marine snail; peptide toxin; inflammation; binding;
KW voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
KW anti-inflammatory.
XX
OS Conus sp.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note= "unspecified"
XX
PN US5994305-A.
XX
PD 30-NOV-1999.
XX
PF 21-AUG-1998; 98US-00138439.
XX
PR 30-DEC-1991; 91US-00814759.
PR 15-APR-1993; 93US-00049794.
PR 03-JUL-1996; 96US-00675354.
PR 01-NOV-1996; 96US-00742774.
XX
XX (ELAN-) ELAN PHARM INC.
XX
PI Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
XX WPI; 2000-038270/03.
XX

```

PT Measuring the activity of test compounds in blocking voltage-gated
PT calcium channels, binding to the omega conopeptide binding site and
PT inhibiting norepinephrine (noradrenaline) release for treating
PT inflammation.

XX Disclosure; Fig 1; 47pp; English.

XX A method has been developed of selecting a test compound for treating
CC inflammation. The method comprises measuring the activity of the test
CC compound in blocking voltage-gated calcium channels, binding to the omega
CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
CC release from nervous tissue. The method is useful for selecting compounds
CC for treating inflammation. The selected compounds are capable of
CC producing analgesia in a mammalian subject with chronic or intractable
CC pain. Analgesia caused by selected compounds may reduce the reliance on
CC opioid analgesic agents of the prior art which cause dependency and
CC tolerance, requiring potentially dangerous increases in opioid doses to
CC achieve the analgesic effect. The present sequence represents an omega
CC conopeptide given in the present invention

XX Sequence 26 AA;

Query Match 57.5%; Score 69; DB 3; Length 26;

Best Local Similarity 34.6%; Pred. No. 22;

Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXCNXXNC 26

| : : : : : | | | | : : : |

Db 1 CKKGACRKTMYDCCSGCGRRGKC 26

RESULT 88

AAy56481

ID AAY56481 standard; peptide; 26 AA.

XX AC AAY56481;

XX DT 16-FEB-2000 (first entry)

XX Natural omega conopeptide MWIIC/SNX-230.

XX Omega conopeptide; analgesic; nociceptive; neuropathic; pain; conotoxin;
KW marine snail; peptide toxin; inflammation; binding;
KW voltage-gated calcium channel; inhibition; norepinephrine; noradrenaline;
KW anti-inflammatory.

XX OS Conus sp.

XX US5994305-A.

XX 30-NOV-1999.

XX 21-AUG-1998; 98US-00138439.

XX 30-DEC-1991; 91US-00814759.

XX 15-APR-1993; 93US-00049794.

XX 03-JUL-1996; 96US-00675354.

XX 01-NOV-1996; 96US-00742774.

XX (ELAN-) ELAN PHARM INC.

XX Justice A, Singh T, Valentino KL, Miljanich GP, Gohl KC;

XX WPI; 2000-038270/03.

XX Measuring the activity of test compounds in blocking voltage-gated
PT calcium channels, binding to the omega conopeptide binding site and
PT inhibiting norepinephrine (noradrenaline) release for treating
PT inflammation.

XX Disclosure; Fig 1; 47pp; English.

XX A method has been developed of selecting a test compound for treating

CC inflammation. The method comprises measuring the activity of the test
CC compound in blocking voltage-gated calcium channels, binding to the omega
CC conopeptide binding site and inhibiting norepinephrine (noradrenaline)
CC release from nervous tissue. The method is useful for selecting compounds
CC for treating inflammation. The selected compounds are capable of
CC producing analgesia in a mammalian subject with chronic or intractable
CC pain. Analgesia caused by selected compounds may reduce the reliance on
CC opioid analgesic agents of the prior art which cause dependency and
CC tolerance, requiring potentially dangerous increases in opioid doses to
CC achieve the analgesic effect. The present sequence represents an omega
CC conopeptide given in the present invention

SQ Sequence 26 AA;

Query Match 57.5%; Score 69; DB 3; Length 26;

Best Local Similarity 30.8%; Pred. No. 22;

Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXCNXXNC 26

| : : : : : | | | | : : : |

Db 1 CKKGACRKTMYDCCSGCGRRGKC 26

RESULT 89

AAy43715

ID AAY43715 standard; peptide; 26 AA.

XX AC AAY43715;

XX DT 11-FEB-2000 (first entry)

XX Amino acid sequence of an omega-conotoxin MWIIC.

XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
KW neuronal damage reduction; ischemia; analgesia; opiate analgesia;
KW schizophrenia; stimulant induced psychosis; hypertension; inflammation;
KW bronchotension; neuropathic pain; voltage sensitive calcium channel.

XX Conus magus.

XX WO9954350-A1.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-AU000288.

XX 16-APR-1998; 98AU-00002989.

XX 01-FEB-1999; 99AU-00008419.

XX (UYQU) UNIV QUEENSLAND.

XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;

XX WPI; 2000-013226/01.

XX Novel peptides used for the treatment of disorders and diseases where
PT blockage of the N-type calcium channels is required.

XX Disclosure; Page 12; 81pp; English.

XX The present sequence represents an omega-conotoxin. Omega-conotoxins are
CC isolated from venoms of predatory marine snails, and have a selectivity
CC for N-type calcium channels over P/Q type channels, and so block N-type
CC calcium channels. The omega-conotoxins of the invention can be used in
CC any disease or disorder where blockage of N-type calcium channels is
CC required, e.g. in the reduction of neuronal damage following ischemia,
CC production of analgesia, or enhancement of opiate analgesia, in the
CC treatment of schizophrenia, stimulant induced psychoses, hypertension,
CC inflammation, and diseases which cause bronchotension, and also in the
CC inhibition of progression of neuropathic pain. They can also be used in a
CC screen to identify compounds with activity at N-type voltage sensitive
CC calcium channels

Query Match	57.5%	Score 69;	DB 3;	Length 26;
Best Local Similarity	34.6%	Pred. No. 22;		


```
Matches 9: Conservative 11: Mismatches 6: Indels 0: Gaps 0:
```

Qy	1	CXIXNQXCQXLD	DDCCSXXCNXXNYC	26
		: :	: :	:
Dp	1	CKGKGAXCRKTM	YDDCCSGSGRRGKC	26

RESULT 92
AAB92220
ID AAB92220 standard; peptide; 26 AA.

AA	AAB92220;
AC	
XX	
DT	22-JUN-2001 (first entry)
XX	
DE	Toxin peptide SEQ ID NO:1396.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS	Homo sapiens.
OS	Synthetic.

PN WO200069900-A2.

23-NOV-2000.

PF 17-MAY-2000; 2000WO-US013576.

PR 17-MAY-1999; 99US-0134406P.

PR 15-OCT-1999; 99US-0159783P.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibadeau K;

DR WPI; 2001-112059/12.

PT Modifying and attaching:

[illegible]

The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidy and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidease stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidease activity *in vivo* for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptideases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptideases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB30829 to AAB92441 represent peptides which can be used in the exemplification of the present invention

Sequence 26 AA;

Query Match 57.5%; Score 69; DB 4; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels

Qy	1	CXIXNQXCQXLDDCCSXXCNXXNC	26
		:	:
	:	:	:
	:	:	:
	:	:	:
	:	:	:
Dp	1	CKKGAPCRKTMYYDCCSGSGRRGKC	26

RESULT 93
AAB19450
ID AAB19450 standard; peptide; 26 AA.
XX
XX AAB19450;
XX AC
XX DT
XX 06-MAR-2001 (first entry)
XX
XX DE Primary sequence of a natural omsqa-conopeptide SNX-231.

Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
peptide toxin; opiate; pain; neuronal damage; ischemic condition;
schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
epilepsy.

05 Conus sp.

Key	Location/Qualifiers
Disulfide-bond	1..16
Modified-site	7
	/label= "Hyp
	/note= "hydroxyproline"
Disulfide-bond	8..20
Disulfide-bond	15..26
Modified-site	26
	/note= "amidated C-terminal"

PN US6136786-A.

PD 24-OCT-2000.

PF 09-SEP-1999; 99US-00392979.

PR 30-DEC-1991; 91US-00814759.

PR 23-JUN-1993; 93US-00081863.

PR 01-NOV-1996; 96US-00742774.

PR 23-APR-1999; 99US-00298017.

PA (ELAN-) ELAN PHARM INC.

PI Singh T, Gohil KC, Valentin

DR WPI; 2001-030946/04.

PT. Enhancing analgesia produced by opiates by administering an o

PT pig ilium and binds to omega-conopeptide MVIIA binding sites in neuronal PT tissues.

PS Disclosure: Fig 1: 58pp: English.

xx The present sequence represents a

are components of peptide toxins which act as voltage-gated channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MW1A binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy.

Sequence 26 AA;

Query Match 57.5%; Score 69; DB 4; Length 26;
Best Local Similarity 30.8%; Pred. No. 22;
Matches 8; Conservative 12; Mismatches 6; Indels

QY 1 CXIXNQXCXQLDDCCSXCNXXNC 26
 | : : : : : | : : : : : | : : : : :
 Db 1 CKGKGPCKRTMYDCCSGCGRRGKC 26

RESULT 94
 AAB19451
 ID AAB19451 standard; peptide; 26 AA.
 AC AAB19451;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE Primary sequence of a natural omega-conopeptide SNX-230.
 XX
 KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.
 XX
 OS Conus sp.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 FT Modified-site 26
 FT /note= "amidated C-terminal"
 XX
 PN US6136786-A.
 XX
 XX 24-OCT-2000.
 PD XX
 XX 09-SEP-1999; 99US-00392979.
 PF XX
 PR 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 23-JUN-1993; 93US-00081863.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 PR 21-AUG-1998; 98US-00138439.
 PR 23-APR-1999; 99US-00298017.
 XX
 FA (ELAN-) ELAN PHARM INC.
 XX
 PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX
 XX WPI; 2001-030946/04.
 XX
 XX Enhancing analgesia produced by opiates by administering an omega-conopeptide that inhibits electrically stimulated contraction of guinea pig ileum and binds to omega-conopeptide MWIIA binding sites in neuronal tissues.
 PT
 PT
 XX
 PS Disclosure; Fig 1; 58pp; English.
 XX
 CC The present sequence represents an omega-conopeptide. Omega-conopeptides are components of peptide toxins which act as voltage-gated calcium channel inhibitors. The peptides are used to enhance the analgesic effect produced by an opiate in a mammalian subject. The method comprises administering to the subject an omega-conopeptide which is able to inhibit electrically stimulated contraction of the guinea pig ileum and bind to omega-conopeptide MWIIA binding sites present in neuronal tissue. Omega-conopeptides are useful for enhancing the analgesic effect produced by an opiate. Omega-conopeptides may also be used in the treatment of pain, in reducing neuronal damage related to an ischemic condition in mammals, and in treating schizophrenia, tardive dyskinesia and acute dystonic reactions, inflammation and epilepsy
 CC
 XX Sequence 26 AA; .

Best Local Similarity 30.8%; Pred No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQLDDCCSXCNXXNC 26
 | : : : : : | : : : : : | : : : : :
 Db 1 CKGKGPCKRTMYDCCSGCGRRGKC 26

RESULT 95
 AAO15125
 ID AAO15125 standard; peptide; 26 AA.
 XX
 AC AAO15125;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Cone snail w-conotoxin peptide MWIIC.
 DE
 KW Cone snail; venomous saliva; calcium channel blocking activity;
 KW stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
 KW w-conotoxin.
 XX
 OS Conus sp.
 XX
 PN JP2002080499-A.
 XX
 PD 19-MAR-2002.
 PF
 XX 01-SEP-2000; 2000JP-00266187.
 XX
 PR 01-SEP-2000; 2000JP-00266187.
 XX
 PA (SUNR) SUNTORY LTD.
 XX
 XX WPI; 2002-421068/45.
 DR
 XX
 PT A new peptide derived from venomous saliva of assassin bug, has calcium channel blocking activity.
 PT
 XX
 PS Disclosure; Page 4; 26pp; Japanese.
 XX
 CC The invention comprises peptides having calcium channel blocking activities which are derived from the venomous saliva of assassin bugs. The calcium channel blocking peptides of the invention are useful for treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral ischaemia. The present amino acid sequence represents a cone snail w-conotoxin peptide
 CC
 XX Sequence 26 AA;
 SQ

Query Match 57.5%; Score 69; DB 5; Length 26;
 Best Local Similarity 30.8%; Pred No. 22;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CXIXNQXCXQLDDCCSXCNXXNC 26
 | : : : : : | : : : : : | : : : : :
 Db 1 CKGKGPCKRTMYDCCSGCGRRGKC 26

RESULT 96
 AAG68252
 ID AAG68252 standard; peptide; 26 AA.
 XX
 AC AAG68252;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Omega-conotoxin MWIIC peptide sequence SEQ ID NO:1.
 XX
 KW Conotoxin; MWIIC; peptide library; disulphide bond; biological activity;
 KW calcium channel blocker.
 XX
 OS Conus sp.

XX FH Key Location/Qualifiers
 FT Disulfide-bond 1. .16
 FT Disulfide-bond 8. .20
 FT Disulfide-bond 15. .26
 FT Modified-site 26
 FT /note= "amidated"
 XX JP2001253899-A.
 XX 18-SEP-2001.
 XX 13-MAR-2000; 2000JP-00068023.
 XX 13-MAR-2000; 2000JP-00068023.
 XX (MITU) MITSUBISHI CHEM CORP.
 XX WPI; 2002-044564/06.
 XX
 XX Manufacturing peptide library, by introducing mutant amino acid in
 XX peptide mixture for synthesizing peptide of interest and its variants,
 XX forming intramolecular disulphide bonds between peptides and separating
 XX them.
 XX Example; Fig 1; 1lpp; Japanese.
 XX The present invention describes a method for manufacturing a peptide
 XX library comprising a peptide (I) having 2 or more intramolecular
 XX disulphide (ID) bonds, and its variants (V). The method comprises
 XX introducing mutant amino acid in the reaction mixture, a peptide mixture
 XX containing two or more amino acids, for chemo-synthesising (I) and (V),
 XX where the ID bonds are formed between the peptides by air oxidation, and
 XX ID-containing peptides are separated. Also described are: (1) a peptide
 XX library obtained by the above said method; (2) screening for mutant
 XX peptide with an improved biological activity than its wild type,
 XX comprising comparing the biological activities of the peptides in the
 XX peptide library with a wild type peptide; (3) a mutant peptide obtained
 XX by the above said screening method; and (4) a calcium channel blocker
 XX containing Omega-conotoxin MVIIIC peptide. The method is useful for
 XX synthesising a peptide library, and for screening peptides with increased
 XX biological activity than the wild type peptides. The method is suitable
 XX for producing many number of variants for a given peptide,
 XX simultaneously. The present sequence represents an omega-conotoxin MVIIIC
 XX peptide which is given in the exemplification of the present invention
 XX
 XX Sequence 26 AA;
 XX
 XX Query Match 57.5%; Score 69; DB 5; Length 26;
 XX Best Local Similarity 30.8%; Pred. No. 22;
 XX Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CXIXNQXCXOXLDCCSXNCNXXNC 26
 Db | : : : : : | | | | : : : : : |
 1 CKGKGPCKRTMYDCCSGCGRRGKC 26
 RESULT 97
 AAW12803
 ID AAW12803 standard; peptide; 29 AA.
 XX AC AAW12803;
 XX 18-APR-1997 (first entry)
 XX Full length omega-conotoxin MVIIIC.
 XX Omega-conotoxin; conus; Conus magus; alpha-conotoxin; mu-conotoxin;
 XX nicotinic acetylcholine receptor; venom; skeletal muscle; inhibitor;
 XX sodium ion channel; presynaptic neuronal calcium ion channel; therapy;
 XX P-like subtype; N-type channel; respiratory rhythm; respiratory control;
 XX neural developmental syndrome; respiratory crisis;
 XX Lambert-Eaton myasthenic syndrome.

XX OS Conus magus.
 XX US5591821-A.
 XX 07-JAN-1997.
 XX 16-JUL-1993; 93US-00092215.
 XX 16-JUL-1993; 93US-00092215.
 XX (UTAH) UNIV UTAH.
 XX Monje VD, Imperial JS, Olivera BM, Hillyard DR;
 XX WPI; 1997-086679/08.
 XX New omega-conotoxin peptide(s) - which target P-type and N-type calcium
 XX ion channels, used for distinguishing calcium channels or for diagnosis.
 XX Example 1; Col 29-30; 2lpp; English.
 XX AAW12800-W12804 represent omega-conotoxins isolated from Conus magus.
 XX This sequence represents the MVIIIC Conus magus omega-conotoxins. Conus
 XX venom contains three types of disulphide rich peptides, these are the
 XX alpha- conotoxins, mu-conotoxins and omega-conotoxins. The alpha-
 XX conotoxins target and block the nicotinic acetylcholine receptors, the mu
 XX conotoxins target and block the skeletal muscle sodium ion channels, and
 XX the omega- conotoxins target and block the presynaptic neuronal calcium
 XX ion channels. The omega-conotoxin peptides of the invention can target P-
 XX like subtypes of calcium ion channels, as well as the N-type channels
 XX (distinguishing them from previously known omega-conotoxins). These
 XX sequences can also be used for distinguishing the types of calcium ion
 XX channels. The presence or absence of sites for the peptides can be
 XX determined in tissue sections, thereby characterising calcium ion channel
 XX expressing cells into various types. As these sequences affect the
 XX control of respiratory rhythms in vivo, they can be used to evaluate
 XX abnormalities in respiratory control which are particularly severe in the
 XX neonatal period. The peptides can also be used for assessing neural
 XX developmental syndromes that result in respiratory crisis, and can be
 XX used to diagnose the Lambert-Eaton myasthenic syndrome
 XX
 XX Sequence 29 AA;
 XX
 XX Query Match 57.5%; Score 69; DB 2; Length 29;
 XX Best Local Similarity 30.8%; Pred. No. 24;
 XX Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 CXIXNQXCXOXLDCCSXNCNXXNC 26
 Db | : : : : : | | | | : : : : : |
 3 CKGKGPCKRTMYDCCSGCGRRGKC 28
 RESULT 98
 ADP04517
 ID ADP04517 standard; protein; 342 AA.
 XX AC ADP04517;
 XX 29-JUL-2004 (first entry)
 XX Sea squirt protein with tissue specific expression in development Seq112.
 XX sea squirt; regeneration medicine; gene therapy; cell proliferation;
 XX differentiation; reproduction; environmental measurement; water survey.
 XX Ciona intestinalis.
 XX JP2004057129-A.
 XX 26-FEB-2004.
 XX 31-JUL-2002; 2002JP-00222593.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:24:17 ; Search time 30.5 Seconds
(without alignments)
66.083 Million cell updates/sec

Title: US-10-627-685A-1
Perfect score: 120
Sequence: 1 CXIXNQXCXQLDCCSXCNXXNXCVCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	81	67.5	26	1	US-07-789-913-19
3	81	67.5	26	1	US-08-049-794-19
4	81	67.5	26	1	US-08-496-847-19
5	81	67.5	26	2	US-08-742-774-19
6	81	67.5	26	2	US-08-675-354-19
7	81	67.5	26	2	US-08-965-918-19
8	81	67.5	26	2	US-08-138-439-19
9	81	67.5	26	3	US-08-613-400A-19
10	81	67.5	26	3	US-08-298-017-19
11	81	67.5	26	3	US-09-392-979A-19
12	77	64.2	26	1	US-07-789-913-8
13	77	64.2	26	1	US-08-049-794-8
14	77	64.2	26	1	US-08-496-847-8
15	77	64.2	26	2	US-08-742-774-8
16	77	64.2	26	2	US-08-675-354-8
17	77	64.2	26	2	US-08-965-918-8
18	77	64.2	26	3	US-09-138-439-8
19	77	64.2	26	3	US-08-613-400A-8
20	77	64.2	26	3	US-08-298-017-8
21	77	64.2	26	3	US-09-392-979A-8
22	72	60.0	2523	1	US-08-185-432-18
23	72	60.0	2523	4	US-08-899-232-3
24	72	60.0	2523	4	US-09-121-457-3
25	69	57.5	26	1	US-08-049-794-21
26	69	57.5	26	1	US-08-049-794-29
27	69	57.5	26	1	US-08-496-847-21

28	69	57.5	26	1	US-08-496-847-29	Sequence 29, Appl
29	69	57.5	26	2	US-08-742-774-21	Sequence 21, Appl
30	69	57.5	26	2	US-08-742-774-29	Sequence 29, Appl
31	69	57.5	26	2	US-08-675-354-21	Sequence 21, Appl
32	69	57.5	26	2	US-08-675-354-29	Sequence 29, Appl
33	69	57.5	26	2	US-08-965-918-21	Sequence 21, Appl
34	69	57.5	26	2	US-08-965-918-29	Sequence 29, Appl
35	69	57.5	26	2	US-09-138-439-21	Sequence 21, Appl
36	69	57.5	26	2	US-09-138-439-29	Sequence 29, Appl
37	69	57.5	26	3	US-08-613-400A-21	Sequence 21, Appl
38	69	57.5	26	3	US-08-613-400A-29	Sequence 29, Appl
39	69	57.5	26	3	US-09-298-017-21	Sequence 21, Appl
40	69	57.5	26	3	US-09-298-017-29	Sequence 29, Appl
41	69	57.5	26	3	US-09-392-979A-21	Sequence 21, Appl
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43	69	57.5	29	1	US-08-092-215-9	Sequence 9, Appl
44	68	56.7	2556	1	US-08-185-432-17	Sequence 17, Appl
45	68	56.7	2556	1	US-08-083-590A-20	Sequence 20, Appl
46	68	56.7	2556	3	US-08-532-384-20	Sequence 20, Appl
47	68	56.7	2556	4	US-08-899-232-2	Sequence 2, Appl
48	68	56.7	2556	4	US-09-121-457-2	Sequence 2, Appl
49	66	55.0	321	4	US-09-270-767-33762	Sequence 33762, A
50	66	55.0	321	4	US-09-270-767-48979	Sequence 48979, A
51	66	55.0	721	3	US-08-872-855-7	Sequence 7, Appl
52	66	55.0	721	3	US-08-981-392-5	Sequence 5, Appl
53	66	55.0	721	4	US-09-908-322-5	Sequence 5, Appl
54	66	55.0	2471	1	US-08-185-432-16	Sequence 16, Appl
55	66	55.0	2471	1	US-08-083-590A-19	Sequence 19, Appl
56	66	55.0	2471	3	US-08-532-384-19	Sequence 19, Appl
57	66	55.0	2471	4	US-08-899-232-1	Sequence 1, Appl
58	66	55.0	2471	4	US-09-121-457-1	Sequence 1, Appl
59	66	55.0	2703	1	US-08-185-432-19	Sequence 19, Appl
60	66	55.0	2703	4	US-08-899-232-4	Sequence 4, Appl
61	66	55.0	2703	4	US-09-121-457-4	Sequence 4, Appl
62	65.5	54.6	36	4	US-09-894-882-168	Sequence 168, App
63	65.5	54.6	36	4	US-09-894-882-369	Sequence 369, App
64	65.5	54.6	73	4	US-09-894-882-167	Sequence 167, App
65	65	54.2	735	3	US-09-191-647-9	Sequence 9, Appl
66	65	54.2	735	3	US-09-540-245A-9	Sequence 9, Appl
67	65	54.2	735	3	US-09-540-153-9	Sequence 9, Appl
68	65	54.2	1964	3	US-09-467-997-1	Sequence 1, Appl
69	65	54.2	2321	4	US-09-230-652-2	Sequence 2, Appl
70	64.5	53.8	32	4	US-09-894-882-364	Sequence 364, App
71	64.5	53.8	35	4	US-09-894-882-413	Sequence 413, App
72	64.5	53.8	71	4	US-09-894-882-119	Sequence 119, App
73	64	53.3	3623	4	US-09-341-461-2	Sequence 2, Appl
74	63.5	52.9	36	4	US-09-894-882-324	Sequence 324, App
75	63.5	52.9	36	4	US-09-894-882-339	Sequence 339, App
76	63.5	52.9	36	4	US-09-894-882-441	Sequence 441, App
77	63.5	52.9	36	4	US-09-894-882-443	Sequence 443, App
78	63.5	52.9	72	4	US-09-894-882-323	Sequence 323, App
79	63.5	52.9	72	4	US-09-894-882-338	Sequence 338, App
80	63	52.5	76	4	US-09-749-637A-207	Sequence 207, App
81	63	52.5	583	4	US-09-641-612-2	Sequence 2, Appl
82	63	52.5	585	4	US-09-641-612-5	Sequence 5, Appl
83	63	52.5	1055	3	US-09-214-278-2	Sequence 2, Appl
84	63	52.5	1055	2	US-09-855-722-2	Sequence 2, Appl
85	63	52.5	1055	2	US-08-400-159-8	Sequence 8, Appl
86	63	52.5	1148	3	US-08-882-046-4	Sequence 4, Appl
87	63	52.5	1148	4	US-09-566-047-4	Sequence 4, Appl
88	63	52.5	1212	3	US-09-214-278-3	Sequence 3, Appl
89	63	52.5	1212	4	US-09-855-722-3	Sequence 3, Appl
90	63	52.5	1238	3	US-09-214-278-5	Sequence 5, Appl
91	63	52.5	1238	4	US-09-855-722-5	Sequence 5, Appl
92	63	52.5	1248	3	US-08-882-046-6	Sequence 6, Appl
93	63	52.5	1248	4	US-09-566-047-6	Sequence 6, Appl
94	63	52.5	1257	3	US-08-611-729A-8	Sequence 8, Appl
95	63	52.5	1257	4	US-09-195-524-8	Sequence 8, Appl
96	62.5	52.1	35	4	US-09-894-882-433	Sequence 433, App
97	62.5	52.1	36	4	US-09-894-882-210	Sequence 210, App
98	62.5	52.1	36	4	US-09-894-882-404	Sequence 404, App
99	62.5	52.1	70	4	US-09-894-882-209	Sequence 209, App
100	62.5	52.1	71	4	US-09-894-882-74	Sequence 74, Appl

ACKNOWLEDGMENTS

APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 19930415
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-049-794-19

Query Match 67.5%; Score 81; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. NO. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCQXLDCCSXCNXXNC 26
Db 1 CKLGQSCSLMYDCCSGCGSGKC 26

RESULT 4

US-08-496-847-19
Sequence 19, Application US/08496847
Patent No. 5795864
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharna
TITLE OF INVENTION: METHODS AND
TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-496-847-19

Query Match 67.5%; Score 81; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. NO. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCQXLDCCSXCNXXNC 26
Db 1 CKLGQSCSLMYDCCSGCGSGKC 26

RESULT 5

US-08-742-774-19
Sequence 19, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/675,354
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444

; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-08-742-774-19

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RESULT 7
US-08-965-918-19
; Street 19, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

```

RESULT 7
US - 08-965-918-19
Sequence 19, Application US/08965918
Patent No. 5991849
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohl, Kishorchandra
APPLICANT: Adriaenssens, Peter I
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND
NUMBER OF INVENTION: PROGRESSION
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dahlinger & Associates
STREET: 350 Cambridge Avenue,
CITY: Palo Alto
STATE: CA

RESULT	7
US-08-96	
; Sequen	
; Patent	
; GENERA	
; APP	
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; APP	
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; TIT	
; NUM	
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; A	
; S	
; C	
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Query Match      67.5%; Score 81; DB 2; Length 26;  
Best Local Similarity 34.6%; Pred. NO. 0.29;  
Matches 9; Conservative 13; Mismatches 4; Indels  
  
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Db       1 CKLKQGCSRLMYDCCSGSCGRSGKC 26  
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RESULT 8  
US-09-138-439-19  
Sequence 19, Application US/09138439  
Patent No. 5994305  
GENERAL INFORMATION.
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; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138.439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-09-138-439-19

Query Match 67.5%; Score 81; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CKLQGQCSRLMYDCCSGCGRSKC 26

RESULT 9
US-08-613-400A-19
; Sequence 19, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA

```

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; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
; US-08-613-400A-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CKLQGQCSRLMYDCCSGCGRSKC 26

RESULT 10
US-09-298-017-19
; Sequence 19, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
Db 1 CKLKGQSCSLMYDCCSGCGSGKC 26

RESULT 11
US-09-392-979A-19
; Sequence 19, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202, FIGURE 2
US-09-298-017-19

Query Match 67.5%; Score 81; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.29;
Matches 9; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQXLDCCSXCNXXNC 26
Db 1 CKLKGQSCSLMYDCCSGCGSGKC 26

RESULT 12
US-07-789-913-8
; Sequence 8, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-183
US-07-789-913-8

Query Match 64.2%; Score 77; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
```



```

RESULT 16
US-08-675-354-8
; Sequence 8, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Deklinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; Zip: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:

```

RESULT 17
 US-08-965-918-8
 ; Sequence 8, Application US/08965918
 ; Patent No. 5891849
 ; GENERAL INFORMATION:
 ; APPLICANT: Amstutz, Gary A.
 ; APPLICANT: Bowersox, Stephen S.
 ; APPLICANT: Gobil, Kishorchandra
 ; APPLICANT: Adriaenssens Peter I.
 ; APPLICANT: Kristipati, Ramasharma
 ; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
 ; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94306-1546
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/965,918
 ; FILING DATE: 07-NOV-1997
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mohr, Judy M.
 ; REGISTRATION NUMBER: 38,563
 ; REFERENCE/DOCKET NUMBER: 5865-0009.34
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880
 ; TELEFAX: 650-324-0960
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
 US-08-965-918-8

; Patent No. 6054429
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Bowersox, S. Scott

APPLICANT: CANNON, Mark, R.
APPLICANT: Pettus, Mark, R.
APPLICANT: Luther, Robert, R.
TITLE OF INVENTION: IMPROVED EPIDURAL

```

CORRESPONDENCE ADDRESS:
ADDRESS: Denlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0

```

```

/ APPLICATION NUMBER: US/09/613,400A
/
/ FILING DATE: 08-MAR-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/

```

ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-613-400A-8

Query Match	64.2%	Score 77	DB 3	Length 26
Best Local Similarity	34.6%	Pred. No. 0.65		
Matches	9	Conservative	12	Mismatches 5
				Indels 0
				Gaps 0

QY	1	CXIXNQXCQXQLDDCCSXXCNXXNC	26
		::: ::: ::: ::: ::: ::: :::	
DB	1	CXIXGASCPKTSVNCSCGSGRSGKC	26

RESULT 20
US-09-298-017-8
US-09-298-017-8

; Sequence 8, Application US/09298017
 ; Patent No. 6087091
 : GENERAL INFORMATION:

Query Match	Score 77;	DB 2;	Length 26;
Best Local Similarity	34.6%;	Pred. No. 0.65;	
Matches	9.	Conservative	12.
	0.	Gaps	5.
	0.	Indels	
APPLICANT:	GOHIL, KISHOR C		
APPLICANT:	VAHINI, KAREN L		
APPLICANT:	SINGH, TEJINDER		
APPLICANT:	SINGH, TEJINDER		
APPLICANT:	SINGH, TEJINDER		

APPLICANT: MILJANICH, GEORGE F
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34

ADDRESSES: Law Offices Of Peter Deminger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA

```
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-09-298-017-8

Query Match 64.2%; Score 77; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXIXNQXCXQXLDCCSXCNXXNC 25
|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 25

RESULT 21
US-09-392-979A-8
; Sequence 8, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-09-298-017-8

Query Match 64.2%; Score 77; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 0.65;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

OY 1 CXIXNQXCXQXLDCCSXCNXXNC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 26

RESULT 22
US-08-185-432-18
; Sequence 18, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-18
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Query Match 60.0%; Score 72; DB 1; Length 2523;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 2 XIXNQXCXOXLDCCSXXCNXXNCV 27
Db 247 GFSGQCNCEINDDCPNNCRNGGTCV 272

RESULT 23

US-08-899-232-3
; Sequence 3, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-08-899-232-3

Query Match 60.0%; Score 72; DB 4; Length 2523;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 2 XIXNQXCXOXLDCCSXXCNXXNCV 27
Db 247 GFSGQCNCEINDDCPNNCRNGGTCV 272

RESULT 24

US-09-121-457-3
; Sequence 3, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2523
; TYPE: PRT
; ORGANISM: Xenopus sp.
US-09-121-457-3

Query Match 60.0%; Score 72; DB 4; Length 2523;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 2 XIXNQXCXOXLDCCSXXCNXXNCV 27
Db 247 GFSGQCNCEINDDCPNNCRNGGTCV 272

RESULT 25

US-08-049-794-21
; Sequence 21, Application US/08049794
; Patent No. 5587454

GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514

Prior Application Data:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-049-794-21

Query Match 57.5%; Score 69; DB 1; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXOXLDCCSXXCNXXNC 26
Db 1 CKGKXACRXTMYDCCSGCGRGKC 26

RESULT 26

US-08-049-794-29
; Sequence 29, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

APPLICATION NUMBER: US/08/436,8
FILING DATE: 27-JUN-1995

MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-496-847-29

Query Match 57.5%; Score 69; DB 1; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXCNXXNC 26
| : : : : : |
Db 1 CKKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 29
US-08-742-774-21
Sequence 21, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-742-774-21

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.8%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXCNXXNC 26
| : : : : : |
Db 1 CKKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 30
US-08-742-774-29
Sequence 29, Application US/08742774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-742-774-29

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXOXLDCCSXCNXXNC 26
| : : : : : |
Db 1 CKKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 31

```

; APPLICANT: MILANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNK-230, FIGURE 1
; US-08-675-354-29

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels

Qy 1 CXTXNXCXOXLDCCSXCNXXNC 26
Db 1 CKGGAPCRKTYDCCSGCRRGKC 26

RESULT 33
US-08-965-918-21
; Sequence 21, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:

```

Sequence 21, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-965-918-21

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSCXCNXXKC 26
Db 1 CKRGAXCRKTMYYCCSGCGRGKC 26

RESULT 34
US-08-965-918-29
Sequence 29, Application US/08965918
Patent No. 5891849
GENERAL INFORMATION:
APPLICANT: Amstutz, Gary A.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Gohil, Kishorchandra
APPLICANT: Adriaenssens, Peter I.
APPLICANT: Kristipati, Ramasharma
TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,918
FILING DATE: 07-NOV-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mohr, Judy M.
REGISTRATION NUMBER: 38,563
REFERENCE/DOCKET NUMBER: 5865-0009.34
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
US-08-965-918-29

Query Match 57.5%; Score 69; DB 2; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSCXCNXXKC 26
Db 1 CKRGAPCRKTMYYCCSGCGRGKC 26

RESULT 35
US-09-138-439-21
Sequence 21, Application US/09138439
Patent No. 5994305
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/138,439
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-04-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
FEATURE:

1 CKGKGAPCRKTMYPDCCSGSGRRGKC 26

US-08-613-400A-29
; Sequence 29, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pattus, Mark, R.
; APPLICANT: Luther, Robert R.

```
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
; US-08-613-400A-29

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 30.8%; Pred. No. 3.4;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDPCSSXXCNXXNC 26
Db 1 CKGKGCXCRKTYDCCSGCGRRGKC 26

RESULT 39
US-09-298-017-21
; Sequence 21, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
```

```
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-298-017-21

Query Match 57.5%; Score 69; DB 3; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDPCSSXXCNXXNC 26
Db 1 CKGKGCXCRKTYDCCSGCGRRGKC 26

RESULT 40
US-09-298-017-29
; Sequence 29, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
```



```
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-20

Query Match      56.7%; Score 68; DB 1; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXNXCVCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 46
US-08-532-384-20
; Sequence 20, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/532.384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-532-384-20

Query Match      56.7%; Score 68; DB 3; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXNXCVCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 47
US-08-899-232-2
; Sequence 2, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-2

Query Match      56.7%; Score 68; DB 4; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXNXCVCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 48
US-09-121-457-2
; Sequence 2, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-2

Query Match      56.7%; Score 68; DB 4; Length 2556;
Best Local Similarity 30.8%; Pred. No. 2.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY      2 XIXNQXCXQXLDCCSXKXCNXNXCVCV 27
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248 GFTGQNCENIDDCPGNCKNGGACV 273

RESULT 49
US-09-270-767-33762
; Sequence 33762, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 82517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33762
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33762
```

Query Match 55.0%; Score 66; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 58;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXCNXXNXC 27
DB 165 TGNQCQTIDDCCASNPCQHGTVC 188

RESULT 50

US-09-270-767-48979
; Sequence 48979, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 48979

; LENGTH: 321

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-48979

Query Match 55.0%; Score 66; DB 4; Length 321;
Best Local Similarity 33.3%; Pred. No. 58;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXCNXXNXC 27
DB 165 TGNQCQTIDDCCASNPCQHGTVC 188

RESULT 51

US-08-872-855-7

; Sequence 7, Application US/08872855

; Patent No. 6121045

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean

; APPLICANT: Gearing, David

; TITLE OF INVENTION: NOVEL HUMAN DELTA3 COMPOSITIONS AND

; TITLE OF INVENTION: THERAPEUTIC USES THEREFOR

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/872,855

; FILING DATE: 11-JUN-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: MAA-003.02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 721 amino acids

;

;

;

;

;

;

;

; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-855-7

Query Match 55.0%; Score 66; DB 3; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXC 26
DB 436 GFSGRNCDDNLDCTSFPCQNGGTC 460

RESULT 52

US-08-981-392-5

; Sequence 5, Application US/08981392

; Patent No. 6262025

; GENERAL INFORMATION:

; APPLICANT: Ish-Horowitz, David

; APPLICANT: Henrique, Domingos Manuel Pinto

; APPLICANT: Lewis, Julian Hart

; APPLICANT: Artavanis-Tsakonas, Spyridon

; APPLICANT: Gray, Grace

; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES

; TITLE OF INVENTION: OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/981,392

; FILING DATE: 22-DEC-1997

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Antler, Adriane M.

; REGISTRATION NUMBER: 32,505

; REFERENCE/DOCKET NUMBER: 7326-038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

; TELEFAX: 212-869-8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 721 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-981-392-5

Query Match 55.0%; Score 66; DB 3; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXCNXXNXC 26
DB 436 GFSGRNCDDNLDCTSFPCQNGGTC 460

RESULT 53

US-09-908-322-5

; Sequence 5, Application US/09908322

Patent No. 6783956
GENERAL INFORMATION:
APPLICANT: Ish-Horowitz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
VERTEBRATE DELTA GENE AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5
Query Match 55.0%; Score 66; DB 4; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQXCXQLDDCCSXCNXNXC 26
DB 436 GFGGRNCDNLDDCTSPFCQNGGTC 460
RESULT 54
US-08-185-432-16
Sequence 16, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
TELECOMMUNICATION INFORMATION:
ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-185-432-16
Query Match 55.0%; Score 66; DB 1; Length 2471;
Best Local Similarity 25.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;
QY 1 CXIXN---QXCXQLDDCCSXCNXNXC 27
DB 324 CVCVNGSGDDCSENIDDCAFASCTPGSTCI 354
RESULT 55
US-08-083-590A-19
Sequence 19, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TELECOMMUNICATION INFORMATION:
Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,590A
FILING DATE: 25-JUN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

Db 2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 63

US-09-894-882-369

Sequence 369, Application US/09894882

Patent No. 6767895

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Walker, Craig S.

APPLICANT: Shetty, Reshma C.

APPLICANT: Jimenez, Elsie C.

APPLICANT: McIntosh, J. Michael

APPLICANT: Olivera, Baldomero M.

APPLICANT: Watkins, Marten

APPLICANT: Jones, Robert M.

APPLICANT: Shen, Greg S.

TITLE OF INVENTION: 1-Superfamily Conotoxins

FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/246,581

PRIOR FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: US 60/247,714

PRIOR FILING DATE: 2000-11-14

PRIOR APPLICATION NUMBER: US 60/264,256

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 506

SOFTWARE: PatentIn version 3.0

SEQ ID NO 369

LENGTH: 36

TYPE: PRT

ORGANISM: Conus betulinus

US-09-894-882-369

Query Match 54.6%; Score 65.5; DB 4; Length 36;

Best Local Similarity 33.3%; Pred. No. 9.2;

Matches 9; Conservative 12; Mismatches 5; Indels 1; Gaps 1;

Qy 1 CXIXNQXCXQXLDCCSXGXCNXXNKCVCV 27

Db 2 CLSLGQRCXRH-SDCCGXLCFFYDKCV 27

RESULT 64

US-09-894-882-167

Sequence 167, Application US/09894882

Patent No. 6767895

GENERAL INFORMATION:

APPLICANT: University of Utah Research Foundation

APPLICANT: Cognetix, Inc.

APPLICANT: Walker, Craig S.

APPLICANT: Shetty, Reshma C.

APPLICANT: Jimenez, Elsie C.

APPLICANT: McIntosh, J. Michael

APPLICANT: Olivera, Baldomero M.

APPLICANT: Watkins, Marten

APPLICANT: Jones, Robert M.

APPLICANT: Shen, Greg S.

TITLE OF INVENTION: 1-Superfamily Conotoxins

FILE REFERENCE: 2314-238

CURRENT APPLICATION NUMBER: US/09/894,882

CURRENT FILING DATE: 2001-06-29

PRIOR APPLICATION NUMBER: US 60/

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 60/243,410

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/246,581

Qy 1 CXIXNQXCXQXLDCCSXGXCNXXNKCVCV 27

Db 39 CLSLGQRCXRH-SDCCGXLCFFYDKCV 64

RESULT 65

US-09-191-647-9

Sequence 9, Application US/09191647

Patent No. 6046015

GENERAL INFORMATION:

APPLICANT: Goodman, Corey

APPLICANT: Kid, Thomas

APPLICANT: Brose, Katja

APPLICANT: Tessier-Lavigne, Marc

TITLE OF INVENTION: Modulating Robo: Ligand Interactions

FILE REFERENCE: B98-031-3

CURRENT APPLICATION NUMBER: US/09/191,647

CURRENT FILING DATE: 1998-11-13

EARLIER APPLICATION NUMBER: 60/065,544

EARLIER FILING DATE: 1997-11-14

EARLIER APPLICATION NUMBER: 60/081,057

EARLIER FILING DATE: 1998-04-07

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

LENGTH: 735

TYPE: PRT

ORGANISM: Caenorhabditis elegans

US-09-191-647-9

Query Match 54.2%; Score 65; DB 3; Length 735;

Best Local Similarity 26.9%; Pred. No. 1.5e+02;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXGXCNXXNKCVCV 27

Db 248 GFEGDYCEKNIDDCVNSKENGKGCVCV 273

RESULT 66

US-09-540-245A-9

Sequence 9, Application US/09540245A

Patent No. 6270984

GENERAL INFORMATION:

APPLICANT: Goodman, Corey

APPLICANT: Kid, Thomas

APPLICANT: Brose, Katja

APPLICANT: Tessier-Lavigne, Marc

TITLE OF INVENTION: Modulating Robo: Ligand Interactions

FILE REFERENCE: B98-031-3

CURRENT APPLICATION NUMBER: US/09/540,245A

CURRENT FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 60/065,544

PRIOR FILING DATE: 1997-11-14

PRIOR APPLICATION NUMBER: 60/081,057

PRIOR FILING DATE: 1998-04-07

<p>; PRIOR FILING DATE: 2001-01-29 ; NUMBER OF SEQ ID NOS: 506 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 364 ; LENGTH: 32 ; TYPE: PRT ; ORGANISM: Conus brunneus US-09-894-882-364</p>	<p>Query Match 53.8%; Score 64.5; DB 4; Length 32; Best Local Similarity 33.3%; Pred. No. 10; Matches 9; Conservative 10; Mismatches 7; Indels 1; Gaps 1;</p>	<p>QY 1 CXIXNQXQXLDDCCSXXCNXXNXCVCV 27 : :: :: :: :: Db 1 CGYVGQACDDD-SDCGSGICCVAGECVCV 26</p>	<p>RESULT 71 US-09-894-882-413 ; Sequence 413, Application US/09894882 ; Patent No. 6767895 ; GENERAL INFORMATION: ; APPLICANT: University of Utah Research Foundation ; APPLICANT: Cognetix, Inc. ; APPLICANT: Walker, Craig S. ; APPLICANT: Shetty, Reshma ; APPLICANT: Jimenez, Elsie C. ; APPLICANT: McIntosh, J. Michael ; APPLICANT: Olivera, Baldomero M. ; APPLICANT: Watkins, Maren ; APPLICANT: Jones, Robert M. ; APPLICANT: Shen, Greg S. ; TITLE OF INVENTION: I-Superfamily Conotoxins ; FILE REFERENCE: 2314-238 ; CURRENT FILING DATE: 2001-06-29 ; PRIOR APPLICATION NUMBER: US 60/ ; PRIOR FILING DATE: 2000-06-30 ; PRIOR APPLICATION NUMBER: US 60/243,410 ; PRIOR FILING DATE: 2000-10-27 ; PRIOR APPLICATION NUMBER: US 60/246,581 ; PRIOR FILING DATE: 2000-11-08 ; PRIOR APPLICATION NUMBER: US 60/247,714 ; PRIOR FILING DATE: 2000-11-14 ; PRIOR APPLICATION NUMBER: US 60/264,256 ; NUMBER OF SEQ ID NOS: 506 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 413 ; LENGTH: 35 ; TYPE: PRT ; ORGANISM: Conus magus US-09-894-882-413</p>	<p>Query Match 53.8%; Score 64.5; DB 4; Length 35; Best Local Similarity 33.3%; Pred. No. 11; Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;</p>	<p>QY 1 CXIXNQXQXLDDCCSXXCNXXNXCVCV 27 : :: :: :: :: Db 3 CSLLGQRCDGH-SDCCWDMCCASEMVCV 28</p>	<p>RESULT 72 US-09-894-882-119 ; Sequence 119, Application US/09894882 ; Patent No. 6767895 ; GENERAL INFORMATION: ; APPLICANT: University of Utah Research Foundation ; APPLICANT: Cognetix, Inc. ; APPLICANT: Walker, Craig S. ; APPLICANT: Shetty, Reshma</p>
<p>; APPLICANT: Jimenez, Elsie C. ; APPLICANT: McIntosh, J. Michael ; APPLICANT: Olivera, Baldomero M. ; APPLICANT: Watkins, Maren ; APPLICANT: Jones, Robert M. ; APPLICANT: Shen, Greg S. ; TITLE OF INVENTION: I-Superfamily Conotoxins ; FILE REFERENCE: 2314-238 ; CURRENT APPLICATION NUMBER: US/09/894,882 ; PRIOR FILING DATE: 2001-06-29 ; PRIOR APPLICATION NUMBER: US 60/ ; PRIOR FILING DATE: 2000-06-30 ; PRIOR APPLICATION NUMBER: US 60/243,410 ; PRIOR FILING DATE: 2000-10-27 ; PRIOR APPLICATION NUMBER: US 60/246,581 ; PRIOR FILING DATE: 2000-11-08 ; PRIOR APPLICATION NUMBER: US 60/247,714 ; PRIOR FILING DATE: 2000-11-14 ; PRIOR APPLICATION NUMBER: US 60/264,256 ; NUMBER OF SEQ ID NOS: 506 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 119 ; LENGTH: 71 ; TYPE: PRT ; ORGANISM: Conus magus US-09-894-882-119</p>	<p>Query Match 53.8%; Score 64.5; DB 4; Length 71; Best Local Similarity 33.3%; Pred. No. 21; Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;</p>	<p>QY 1 CXIXNQXQXLDDCCSXXCNXXNXCVCV 27 : :: :: :: :: Db 39 CSLLGQRCDGH-SDCCWDMCCASEMVCV 64</p>	<p>RESULT 73 US-09-341-461-2 ; Sequence 2, Application US/09341461 ; Patent No. 6586389 ; GENERAL INFORMATION: ; APPLICANT: Hammond, Timothy G. ; APPLICANT: Vertoust, Pierre J. ; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin ; TITLE OF INVENTION: and Uses Thereof ; FILE REFERENCE: D6148 ; CURRENT APPLICATION NUMBER: US/09/341,461 ; CURRENT FILING DATE: 2000-07-20 ; PRIOR APPLICATION NUMBER: PCT/US99/01259 ; PRIOR FILING DATE: 1999-01-21 ; NUMBER OF SEQ ID NOS: 40 ; SEQ ID NO 2 ; LENGTH: 3623 ; TYPE: PRT ; ORGANISM: rat ; FEATURE: ; OTHER INFORMATION: amino acid sequence of rat cubilin protein US-09-341-461-2</p>	<p>Query Match 53.3%; Score 64; DB 4; Length 3623; Best Local Similarity 29.2%; Pred. No. 7.5e+02; Matches 7; Conservative 13; Mismatches 4; Indels 0; Gaps 0;</p>	<p>QY 4 XNOQCXQXLDDCCSXXCNXXNXCVCV 27 : :: :: :: :: Db 425 SGONCTENINCSNPCLNGGTCTI 448</p>	<p>RESULT 74 US-09-894-882-324 ; Sequence 324, Application US/09894882 ; Patent No. 6767895</p>

RESULT 77
US-09-894-882-443

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RESULT 78
// SEQUENCE 894-882-323
// - Sequence 323, Application US/09894882
// Patent No. 6767895
//
// GENERAL INFORMATION:
// APPLICANT: University of Utah Research Foundation
// APPLICANT: Cognetix, Inc.
// APPLICANT: Walker, Craig S.
// APPLICANT: Shetty, Reshma
// APPLICANT: Jimenez, Elsie C.
// APPLICANT: McIntosh, J. Michael
// APPLICANT: Olivera, Baldomero M.
// APPLICANT: Watkins, Maren
// APPLICANT: Jones, Robert M.
// APPLICANT: Shen, Greg S.
//
// TITLE OF INVENTION: I-Superfamily Conotoxins
//
// FILE REFERENCE: 2314-238
//
// CURRENT APPLICATION NUMBER: US/09/894,882
//
// CURRENT FILING DATE: 2001-06-29
//
// PRIOR APPLICATION NUMBER: US 60/
//
// PRIOR FILING DATE: 2000-06-30
//
// PRIOR APPLICATION NUMBER: US 60/243,410
//
// PRIOR FILING DATE: 2000-10-27
//
// PRIOR APPLICATION NUMBER: US 60/246,581
//
// PRIOR FILING DATE: 2000-11-08
//
// PRIOR APPLICATION NUMBER: US 60/247,714
//
// PRIOR FILING DATE: 2000-11-14
//
// PRIOR APPLICATION NUMBER: US 60/264,256
//
// PRIOR FILING DATE: 2001-01-29

```

APPLICANT: Cartier, G. Edward

APPLICANT: Carter, G. Edward
; APPLICANT: Watkins, Maren

```
; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 207
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Conus distans
US-09-749-637A-207

Query Match      52.5%; Score 63; DB 4; Length 76;
Best Local Similarity 35.7%; Pred. No. 30;
Matches 10; Conservative 12; Mismatches 4; Indels 4; Gaps 2;

QY 1 CXIXNQXCXQXLDCCSXKN-XXNXCV 27
| : : : : : | : : : : : | : : : : : | : : : : : |
Db 48 CNEAQEHCTQN-PDCCSESCNKFVGRCL 74

RESULT 81
US-09-641-612-2
; Sequence 2, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-2

Query Match      52.5%; Score 63; DB 4; Length 583;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 378 GFAGPRCEHLDLDDCAGCANGGTCTV 403

RESULT 82
US-09-641-612-5
; Sequence 5, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

; APPLICANT: Hillyard, David R.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Layer, Richard M.
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
; FILE REFERENCE: 2314-227
; CURRENT APPLICATION NUMBER: US/09/749,637A
; CURRENT FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/243,412
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US60/219,440
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/214,263
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/173,754
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 409
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 207
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: VARIANT
; LOCATION: (1)...(585)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-641-612-5

Query Match      52.5%; Score 63; DB 4; Length 585;
Best Local Similarity 30.8%; Pred. No. 1.8e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 380 GFAGPRCEHLDLDDCAGCANGGTCTV 405

RESULT 83
US-09-214-278-2
; Sequence 2, Application US/09214278
; Patent No. 6291210
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/214,278
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-278-2

Query Match      52.5%; Score 63; DB 3; Length 1055;
Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
Db 601 GFTGTYCHENIDDLCLGQPCRNNGGTCTI 626

RESULT 84
US-09-855-722-2
; Sequence 2, Application US/09855722
; Patent No. 6638741
; GENERAL INFORMATION:
; APPLICANT: Sakano, Seiji
; APPLICANT: Itoh, Akira
; TITLE OF INVENTION: DIFFERENTIATION-SUPPRESSIVE POLYPEPTIDE
; FILE REFERENCE: KP-8576
; CURRENT APPLICATION NUMBER: US/09/855,722
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/214,278
; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1055
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-722-2

Query Match      52.5%; Score 63; DB 4; Length 1055;
Best Local Similarity 23.1%; Pred. No. 3.1e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXKNXXNXCV 27
: : : : : | : : : : : | : : : : : | : : : : : |
```

Db 601 GFTGTYCHENIDDLGQPCRNNGTCTI 626

RESULT 85

US-08-400-159-8

Sequence 8, Application US/08400159

Patent No. 5869282

GENERAL INFORMATION:

APPLICANT: Ish-Horowitz, David

APPLICANT: Henrique, Domingos M.P.

APPLICANT: Lewis, Julian H.

APPLICANT: Myat, Anna M.

APPLICANT: Fleming, Robert J.

APPLICANT: Artavanis-Tsakonas, Spyridon

APPLICANT: Mann, Robert S.

APPLICANT: Gray, Grace E.

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE

TITLE OF INVENTION: SRRATE GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,159

FILING DATE: 07-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 7326-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1065 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-400-159-8

Query Match 52.5%; Score 63; DB 2; Length 1065;

Best Local Similarity 23.1%; Pred. No. 3.le+02;

Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDLDCSCXCNXNXCVCV 27

Db 457 GFTGTYCHENIDDLGQPCRNNGTCTI 482

RESULT 86

US-08-882-046-4

Sequence 4, Application US/08882046

Patent No. 6136952

GENERAL INFORMATION:

APPLICANT: Li, Linheng

APPLICANT: Hood, Leroy

APPLICANT: Krantz, Ian D.

APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Human Jagged Polypeptide, Encoding

TITLE OF INVENTION: Nucleic Acids and Methods of Use

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/566,047

FILING DATE: 05-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/882,046

FILING DATE: 25-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

Query Match 52.5%; Score 63; DB 3; Length 1148;

Best Local Similarity 23.1%; Pred. No. 3.3e+02;

Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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Db 538 GFTGTYCHENIDDLGQPCRNNGTCTI 563

RESULT 87

US-09-566-047-4

Sequence 4, Application US/09566047

Patent No. 6703198

GENERAL INFORMATION:

APPLICANT: Li, Linheng

APPLICANT: Hood, Leroy

APPLICANT: Krantz, Ian D.

APPLICANT: Spinner, Nancy B.

TITLE OF INVENTION: Methods of Diagnosing Alagille Syndrome

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/566,047

FILING DATE: 05-May-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/882,046

FILING DATE: 25-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815


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; APPLICANT: Spinner, Nancy B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UW 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9901
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-882-046-6

Query Match 52.5%; Score 63; DB 3; Length 1248;
Best Local Similarity 23.1%; Pred. No. 3.6e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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RESULT 93
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; Patent No. 6703198
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; Hood, Leroy
; Krantz, Ian D.
; Spinner, Nancy B.
; TITLE OF INVENTION: Methods of Diagnosing Alegillie Syndrome
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/566,047
; FILING DATE: 05-May-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/882,046
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; FILING DATE: 25-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UW 4164
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (858) 535-9901
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-566-047-6

Query Match 52.5%; Score 63; DB 4; Length 1248;
Best Local Similarity 23.1%; Pred. No. 3.6e+02;
Matches 6; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXKXCV 27
Db 628 GFTGTYCHENIDDCMGQPCRNGGTCT 653

RESULT 94
US-08-611-729A-8
; Sequence 8, Application US/08611729A
; Patent No. 6004924
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; APPLICANT: Henrique, Domingos M.P.
; APPLICANT: Lewis, Julian H.
; APPLICANT: Myat, Anna M.
; APPLICANT: Fleming, Robert J.
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Mann, Robert S.
; APPLICANT: Gray, Grace E.
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF THE
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,729A
; FILING DATE: 06-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-611-729A-8
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; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 210
; LENGTH: 36
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; ORGANISM: Conus lynceus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: Xaa at residues 2 and 4 is Trp or bromo-Trp; Xaa at residue 25 is
; OTHER INFORMATION: Tyr, 125i-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
; OTHER INFORMATION: spho-Ty
US-09-894-882-210

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Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

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Db 5 CFNAGVKCDNH-SDCCADTCCYDNTCV 30

RESULT 98
US-09-894-882-404
; Sequence 404, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-404

Query Match          52.1%; Score 62.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 17;
Matches 10; Conservative 10; Mismatches 6; Indels 1; Gaps 1;

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; Sequence 209, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
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; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
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; SEQ ID NO 209
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Conus lynceus
US-09-894-882-209

Query Match          52.1%; Score 62.5; DB 4; Length 70;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

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; Sequence 74, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
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; TYPE: PRT
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US-09-894-882-74

Query Match 52.1%; Score 62.5; DB 4; Length 71;
Best Local Similarity 33.3%; Pred. No. 31;
Matches 9; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

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Db 39 CSFLGQCGDH-SDCCWNMCCASEMCV 64

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 20:29:42 ; Search time 91.5 Seconds
(without alignments)
98.077 Million cell updates/sec

Title: US-10-627-685A-1
Perfect score: 120
Sequence: 1 CXIXNQXQXQLDDCCSXCNXXNCV 27

Scoring table: BLOSUM62DX
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Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_PUB.pdb.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pdb.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 2, Appli
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Sequence 57, Appl
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Sequence 723, App
Sequence 168, App
Sequence 369, App
Sequence 167, App
Sequence 699, Ap
Sequence 9, Appli
Sequence 26, Appl
Sequence 26, Appl

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 2, 7, 18, 19, 22 and 25 may be Arg,
; OTHER INFORMATION: homocysteine, ornithine, Lys, N-methyl-Lys,
; OTHER INFORMATION: N,N-dimethyl-Lys, N,N-trimethyl-Lys, any
; OTHER INFORMATION: synthetic basic amino acid, His or halo-His; Xaa
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: at residue 4 may be Pro or Hyp; Xaa at residue 9 and
; OTHER INFORMATION: 23 may be Phe-Tyr, meta-Tyr, ortho-Tyr, nor-Tyr,
; OTHER INFORMATION: mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
; OTHER INFORMATION: O-phospho-Tyr, nitro-Tyr, Trp (D or L),
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: neo-Trp,halo-Trp (D or L) or any synthetic aromatic amino
; OTHER INFORMATION: acid; Xaa at residue 11 is His or halo-His
US-10-352-254-1

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXNXCVCV 27
DB 1 CXIXNQXCXQXLDCCSXXCNXXNXCVCV 27

RESULT 2
US-10-352-254-2
; Sequence 2, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-2

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
QY 1 CXIXNQXCXQXLDCCSXXCNXXNXCVCV 27
DB 1 CRXNQKCFQHLDDCCSAKCNRFKVCV 27

RESULT 3
US-10-352-254-3
; Sequence 3, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCXV 27

RESULT 4

US-10-352-254-5
; Sequence 5, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-5

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCXV 27

RESULT 5

US-10-352-254-6
; Sequence 6, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-6

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCXV 27

RESULT 6

US-10-352-254-7
; Sequence 7, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-7

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNKCXV 27
Db 1 CRIXNQKCAQHLDDCCSRKCNRFNKCXV 27

RESULT 7

US-10-352-254-8
; Sequence 8, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; PRIOR FILING DATE: 2003-01-28
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRP
; ORGANISM: Conus purpurascens
US-10-352-254-8

<p>; FEATURE: ; NAME/KEY: PEPTIDE ; LOCATION: (1)..(27) ; OTHER INFORMATION: Xaa is Hyp</p>	<p>US-10-352-254-8</p>
Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY	1 CXIXNQXCXQLDDCCSXKCNXXNKCV 27
DB	1 CRINXQCFQHLLDCCSRKNRFNKCVCV 27
RESULT 8	
US-10-352-254-9	
Sequence 9, Application US/10352254	
Publication No. US20030224343A1	
GENERAL INFORMATION:	
APPLICANT: Cognetix, Inc.	
APPPLICANT: University of Utah Research Foundation	
APPLICANT: Pemberton-Goodman, Karen	
APPLICANT: Jones, Robert M.	
APPLICANT: Temple, Davis	
APPLICANT: McIntosh, J. Michael	
APPLICANT: Olivera, Baldomero M.	
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants	
FILE REFERENCE: 2314-254	
CURRENT APPLICATION NUMBER: US/10/352,254	
CURRENT FILING DATE: 2003-01-28	
PRIOR APPLICATION NUMBER: US 60/352,219	
PRIOR FILING DATE: 2002-01-29	
NUMBER OF SEQ ID NOS: 28	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 9	
LENGTH: 27	
TYPE: PRT	
ORGANISM: Conus purpurascens	
FEATURE:	
NAME/KEY: PEPTIDE	
LOCATION: (1)..(27)	
OTHER INFORMATION: Xaa is Hyp	
US-10-352-254-9	
Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY	1 CXIXNQXCXQLDDCCSXKCNXXNKCV 27
DB	1 CRINXQCFQHLLDCCSRKNRFNKCVCV 27
RESULT 9	
US-10-352-254-10	
Sequence 10, Application US/10352254	
Publication No. US20030224343A1	
GENERAL INFORMATION:	
APPLICANT: Cognetix, Inc.	
APPLICANT: University of Utah Research Foundation	
APPLICANT: Pemberton-Goodman, Karen	
APPLICANT: Jones, Robert M.	
APPLICANT: Temple, Davis	
APPLICANT: McIntosh, J. Michael	
APPLICANT: Olivera, Baldomero M.	
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants	
FILE REFERENCE: "2314-254"	
CURRENT APPLICATION NUMBER: US/10/352,254	
CURRENT FILING DATE: 2003-01-28	
PRIOR APPLICATION NUMBER: US 60/352,219	
PRIOR FILING DATE: 2002-01-29	
NUMBER OF SEQ ID NOS: 28	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 10	
LENGTH: 27	
TYPE: PRT	
ORGANISM: Conus purpurascens	
FEATURE:	
NAME/KEY: PEPTIDE	
LOCATION: (1)..(27)	
OTHER INFORMATION: Xaa is Hyp	
US-10-352-254-9	
Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY	1 CXIXNQXCXQLDDCCSXKCNXXNKCV 27
DB	1 CRINXQCFQHLLDCCSRKNRFNKCVCV 27
RESULT 10	
US-10-352-254-11	
Sequence 11, Application US/10352254	
Publication No. US20030224343A1	
GENERAL INFORMATION:	
APPLICANT: Cognetix, Inc.	
APPLICANT: University of Utah Research Foundation	
APPLICANT: Pemberton-Goodman, Karen	
APPLICANT: Jones, Robert M.	
APPLICANT: Temple, Davis	
APPLICANT: McIntosh, J. Michael	
APPLICANT: Olivera, Baldomero M.	
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants	
FILE REFERENCE: 2314-254	
CURRENT APPLICATION NUMBER: US/10/352,254	
CURRENT FILING DATE: 2003-01-28	
PRIOR APPLICATION NUMBER: US 60/352,219	
PRIOR FILING DATE: 2002-01-29	
NUMBER OF SEQ ID NOS: 28	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 11	
LENGTH: 27	
TYPE: PRT	
ORGANISM: Conus purpurascens	
FEATURE:	
NAME/KEY: PEPTIDE	
LOCATION: (1)..(27)	
OTHER INFORMATION: Xaa is Hyp	
US-10-352-254-11	
Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY	1 CXIXNQXCXQLDDCCSXKCNXXNKCV 27
DB	1 CRINXQCFQHLLDCCSRKNRFNKCVCV 27
RESULT 11	
US-10-352-254-12	
Sequence 12, Application US/10352254	
Publication No. US20030224343A1	
GENERAL INFORMATION:	
APPLICANT: Cognetix, Inc.	
APPLICANT: University of Utah Research Foundation	
APPLICANT: Pemberton-Goodman, Karen	
APPLICANT: Jones, Robert M.	
APPLICANT: Temple, Davis	
APPLICANT: McIntosh, J. Michael	
APPLICANT: Olivera, Baldomero M.	
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants	
FILE REFERENCE: "2314-254"	
CURRENT APPLICATION NUMBER: US/10/352,254	
CURRENT FILING DATE: 2003-01-28	
PRIOR APPLICATION NUMBER: US 60/352,219	
PRIOR FILING DATE: 2002-01-29	
NUMBER OF SEQ ID NOS: 28	
SOFTWARE: PatentIn Ver. 2.0	
SEQ ID NO 12	
LENGTH: 27	
TYPE: PRT	
ORGANISM: Conus purpurascens	
FEATURE:	
NAME/KEY: PEPTIDE	
LOCATION: (1)..(27)	
OTHER INFORMATION: Xaa is Hyp	
US-10-352-254-11	
Query Match Best Local Similarity 100.0%; Score 120; DB 15; Matches 66.7%; Pred. No. 4.7e-05;	<p>Mismatches 9; Indels 0; Gaps 0;</p>
QY	1 CXIXNQXCXQLDDCCSXKCNXXNKCV 27
DB	1 CRINXQCFQHLLDCCSRKNRFNKCVCV 27

; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-12

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRIXNQCYQHLDCCSRKCNRFNKCVCV 27

RESULT 12
US-10-352-254-13
; Sequence 13, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-13

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CQIXNQCFQHLDCCSRKCNRFNKCVCV 27

RESULT 13
US-10-352-254-14
; Sequence 14, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.

; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-14

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRIXNQCFQHLDCCSRKCNRFNKCVCV 27

RESULT 14
US-10-352-254-24
; Sequence 24, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-352-254-24

Query Match 100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 4.7e-05;
Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXXNKCVCV 27
|:||||:|:||||:|:||||:|:||||:|
Db 1 CRIANQCFQHLDCCSRKCNRFNKCVCV 27

RESULT 15
US-10-627-685-1
; Sequence 1, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-2

Query Match      100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY    1 CXIXNQXCXQLDDCCSXXCNXXNKCV 27
       |:|::|:|:|:|:|:|:|:|:|:|:|
Db    1 CRIXNKCFCQLHDDCCSRKCNFKNKV 27

RESULT 17
US-10-627-685-3
; Sequence 3, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-3

Query Match      100.0%; Score 120; DB 15; Length 27;
Best Local Similarity 66.7%; Pred. No. 4.7e-05;
Matches 18; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY    1 CXIXNQXCXQLDDCCSXXCNXXNKCV 27
       |:|::|:|:|:~::~||:|:|:|
Db    1 CRIXNKCFCQLHDDCCSRKCNFKNKV 27

RESULT 18
US-10-627-685-5
; Sequence 5, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
```


GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23

Query Match 96.7%; Score 116; DB 15; Length 27;
Best Local Similarity 65.4%; Pred. No. 0.00011;
Matches 17; Conservative 9; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNC 26
DB 1 CRXNQKCFQHLDDCCSRKCNRFNC 26

RESULT 33
US-10-352-254-4
; Sequence 4, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-4

Query Match 95.8%; Score 115; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00014;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNCV 27

RESULT 34
US-10-352-254-20
; Sequence 20, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20

Query Match 95.8%; Score 115; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00014;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXXCNXXNCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNCV 27

RESULT 35
US-10-627-685-4
; Sequence 4, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:

[illegible]


```
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27
   |::|||::|||::|||::|||::|||::|||
Db 1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27

RESULT 47
US-10-627-685-17
; Sequence 17, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27
   |::|||::|||::|||::|||::|||::|||
Db 1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27

RESULT 48
US-10-627-685-19
; Sequence 19, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
```

```
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27
   |::|||::|||::|||::|||::|||::|||
Db 1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27

RESULT 49
US-10-627-685-21
; Sequence 21, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27
   |::|||::|||::|||::|||::|||::|||
Db 1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27

RESULT 49
US-10-627-685-21
; Sequence 21, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21

Query Match          93.3%; Score 112; DB 15; Length 27;
Best Local Similarity 63.0%; Pred. No. 0.00028;
Matches 17; Conservative 9; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27
   |::|||::|||::|||::|||::|||::|||
Db 1 CRIXNQKCFQHLDDCCSRKCNRFKCV 27
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[illegible]


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; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
; OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr
US-10-765-926-268

Query Match 58.3%; Score 70; DB 16; Length 26;
Best Local Similarity 34.6%; Pred. No. 3.2;
Matches 9; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXIXNQXQXQLDDCCSXXCNXXNXC 26
   : : : : : : : : : : : : : : : : : :
Db 1 CKLKGQSCRKTXDCSCSGSGRSGKC 26

RESULT 61
US-09-944-849-2
; Sequence 2, Application US/09944849
; Patent No. US20020151487A1
; GENERAL INFORMATION:
; APPLICANT: Nickoloff, Brian
; APPLICANT: Mele, Lucio
; TITLE OF INVENTION: METHOD AND REAGENTS FOR EPITHELIAL BARRIER FORMATION AND TREATMENT OF SKIN DISORDERS
; TITLE OF INVENTION: MALIGNANT AND BENIGN SKIN DISORDERS BY MODULATING THE NOTCH SIGNALING PATHWAY
; FILE REFERENCE: 212583
; CURRENT APPLICATION NUMBER: US/09/944,849
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,614
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (891)..(891)
; OTHER INFORMATION: The 'Xaa' at location 891 stands for Gly, or Ala.
; NAME/KEY: misc feature
; LOCATION: (1763)..(1763)
; OTHER INFORMATION: The 'Xaa' at location 1763 stands for Gln, Arg, Pro, or Leu.
; NAME/KEY: misc feature
; LOCATION: (1787)..(1787)
; OTHER INFORMATION: The 'Xaa' at location 1787 stands for Thr, Ala, Pro, or Ser.
; OTHER INFORMATION: Constitutively Active No. US20020151487A1ch-1
US-09-944-849-2

Query Match 56.7%; Score 68; DB 9; Length 2444;
Best Local Similarity 30.8%; Pred. No. 3.4e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXXCNXXNXC 27
   : : : : : : : : : : : : : : : : : :
Db 248 GTFGQNCENIDDCPNCKNGGACV 273

RESULT 62
US-10-072-012-469
; Sequence 469, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara

```



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/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zerhusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Guev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072.012

```

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/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zerkusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: Proteins and Nucleic
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30

```

US-10-765-727-22

Query Match 56.7%; Score 68; DB 17; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXXCNXXNKCVCV 27
DB 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 68

US-10-846-989-56
Sequence 56, Application US/10846989
Publication No. US20050026831A1
GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: LENNARD, ANDREW CHRISTOPHER
APPLICANT: MCKENZIE, GRAHAME JAMES
APPLICANT: RAGNO, SILVIA
APPLICANT: TUGAL, TAMARA
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MEDICAL TREATMENT
FILE REFERENCE: 654525-2012
CURRENT APPLICATION NUMBER: US/10/846,989
PRIOR FILING DATE: 2004-05-14
PRIOR APPLICATION NUMBER: PCT/GB02/05133
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: GB 0127271.5
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: GB 0220913.8
PRIOR FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 56
LENGTH: 2556
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (891)
OTHER INFORMATION: Variable amino acid

US-10-846-989-56

Query Match 56.7%; Score 68; DB 17; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXXCNXXNKCVCV 27
DB 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 69

US-10-764-415B-39
Sequence 39, Application US/10764415B
Publication No. US20050059093A1
GENERAL INFORMATION:
APPLICANT: LoranTis Ltd.
TITLE OF INVENTION: Modulations of Notch signalling for use in Immunotherapy
FILE REFERENCE: P0110730US
CURRENT APPLICATION NUMBER: US/10/764,415B
PRIOR FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: GB0118153.6
PRIOR FILING DATE: 2001-07-01
PRIOR APPLICATION NUMBER: GB0207930.9
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB0212283.6
PRIOR FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: GB0212282.8
PRIOR FILING DATE: 2002-05-28

US-10-765-727-22

Query Match 56.7%; Score 68; DB 15; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXXCNXXNKCVCV 27
DB 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 67

US-10-765-727-22
Sequence 22, Application US/10765727
Publication No. US20050025751A1
GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
FILE REFERENCE: 674525-2010
CURRENT APPLICATION NUMBER: US/10/765,727
PRIOR FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: PCT/GB02/03426
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: GB 0118153.6
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: GB 0207930.9
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB 0212282.8
PRIOR FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: GB 0212283.6
PRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 22
LENGTH: 2556
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (891)
OTHER INFORMATION: Variable amino acid

US-10-072-012-467

Query Match 56.7%; Score 68; DB 15; Length 2556;
Best Local Similarity 30.8%; Pred. No. 3.5e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXXCNXXNKCVCV 27
DB 248 GFTGQNCENIDDCPGNNCKNGGACV 273

RESULT 67

US-10-765-727-22
Sequence 22, Application US/10765727
Publication No. US20050025751A1
GENERAL INFORMATION:
APPLICANT: BODMER, MARK WILLIAM
APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
APPLICANT: CHAMPION, BRIAN ROBERT
APPLICANT: YOUNG, LESLEY LYNN
TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
FILE REFERENCE: 674525-2010
CURRENT APPLICATION NUMBER: US/10/765,727
PRIOR FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: PCT/GB02/03426
PRIOR FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: GB 0118153.6
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: GB 0207930.9
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: GB 0212282.8
PRIOR FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: GB 0212283.6
PRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 22
LENGTH: 2556
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (891)
OTHER INFORMATION: Variable amino acid

Db 248 GFAGQCEENVDDCPGNCKNGGACV 273

RESULT 74

US-09-910-082A-149
; Sequence 149, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(29)
; OTHER INFORMATION: Xaa at residue 4, and 7 is Pro or Hyp; Xaa at residue 22 and 29 is
; OTHER INFORMATION: Tyr, 125i-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-pho
US-09-910-082A-149

Query Match 55.0%; Score 66; DB 10; Length 29;

Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDCCSXXCNXXNXC 26

Db 1 CKSXGTXCGRMRDCCCTCLSLXSNKC 26

RESULT 75

US-10-765-926-149
; Sequence 149, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 149
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Conus geographus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(29)
; OTHER INFORMATION: Xaa at residue 4 and 7 is Pro or Hyp; Xaa at
; OTHER INFORMATION: residue 22 and 29 is Tyr, 125i-Tyr, mono-iodo-Tyr,
; OTHER INFORMATION: di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Tyr
US-10-765-926-149

Query Match 55.0%; Score 66; DB 16; Length 29;

Best Local Similarity 38.5%; Pred. No. 8.7;
Matches 10; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXIXNOXCXQXLDCCSXXCNXXNXC 26

Db 1 CKSXGTXCGRMRDCCCTCLSLXSNKC 26

RESULT 76

US-10-024-599-4
; Sequence 4, Application US/10024599
; Publication No. US20020165352A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Cimbora, Daniel M.
; APPLICANT: Heichman, Karen
; APPLICANT: Bartel, Paul L.
; TITLE OF INVENTION: Protein-Protein Interactions
; FILE REFERENCE: 2318-278-II
; CURRENT APPLICATION NUMBER: US/10/024,599
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/256,986
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: 1..176
; OTHER INFORMATION: Xaa is Gly or Cys
US-10-024-599-4

Query Match 55.0%; Score 66; DB 13; Length 176;

Best Local Similarity 25.8%; Pred. No. 46;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

Qy 1 CXIXN----QXCXQXLDCCSXXCNXXNXC 27

Db 9 CVCVNGWSGDCCSENIDDCAFASCTPGSTCI 39

RESULT 77

US-09-908-322-5
; Sequence 5, Application US/09908322
; Patent No. US20020107194A1
; GENERAL INFORMATION:
; APPLICANT: Ish-Horowitz, David
; Henrique, Domingos Manuel Pinto
; Lewis, Julian Hart
; Artavanis-Tsakonas, Spyridon
; Gray, Grace
; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF
; VERTEBRATE DELTA GENE AND METHODS BASED THEREON
; NUMBER OF SEQUENCES: 94

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirostock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5

Query Match 55.0%; Score 66; DB 9; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQLDDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSFPCQNGGTC 460

RESULT 78
US-09-783-931-5
Sequence 5, Application US/09783931
Publication No. US20030073620A1
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
Henrique, Domingos Manuel Pinto
Lewis, Julian Hart
Artavanis-Tsakonas, Spyridon
Gray, Grace
TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/783,931

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,322
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/981,392
FILING DATE: 22-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mirostock, S Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 721 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-908-322-5

Query Match 55.0%; Score 66; DB 9; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQLDDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSFPCQNGGTC 460

RESULT 79
US-10-417-719-7
Sequence 7, Application US/10417719
Publication No. US20030180784A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc
APPLICANT: McCarthy, Sean
APPLICANT: Gearing, David
TITLE OF INVENTION: HUMAN DELTA3 AND USES THEREOF
FILE REFERENCE: MB101997-002CP2M
CURRENT APPLICATION NUMBER: US/10/417,719
CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/568,218
PRIOR FILING DATE: 2000-05-09
PRIOR APPLICATION NUMBER: 08/872,855
PRIOR FILING DATE: 1997-06-11
PRIOR APPLICATION NUMBER: 08/832,633
PRIOR FILING DATE: 1997-04-04
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 721
TYPE: PRT
ORGANISM: Xenopus laevis
US-10-417-719-7

Query Match 55.0%; Score 66; DB 14; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQLDDCCSXCNXXNXC 26
Db 436 GFSGRNCDNLDCTSFPCQNGGTC 460

RESULT 80
US-10-042-865-109
Sequence 109, Application US/10042865
Publication No. US20040029216A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
```

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; APPLICANT: Li, Li
; APPLICANT: Zerkhusen, Bryan D
; APPLICANT: Caaman, Stacie J
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zhong, Mei
; APPLICANT: Gangolli, Esha A
; APPLICANT: Burgess, Catherine E
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Taylor, Sarah
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Miller, Charles E
; APPLICANT: Guo, Xiaojia
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gerlach, Valerie L
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Millet, Isabelle
; APPLICANT: Payman, John
; APPLICANT: Smithson, Glennnda
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, David
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-537
; CURRENT APPLICATION NUMBER: US/10/042,865
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/260,417
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/260,831
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/272,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/274,876
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/284,704
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 264
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 109
; LENGTH: 721
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-042-865-109

Query Match 55.0%; Score 66; DB 15; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.7e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXXCNXNXC 26
: : : : : : : : : : : : : : : :
Db 436 GFGSRNCDDNLDCTSPFCQNGTC 460

RESULT 81
US-10-190-115-4
; Sequence 4, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Caaman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
```

```
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 4
; LENGTH: 1473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-4

Query Match 55.0%; Score 66; DB 15; Length 1473;
Best Local Similarity 25.8%; Pred. No. 3.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXXCNXNXC 27
: : : : : : : : : : : : : : : :
Db 324 CVCVNGWSGDCSENIDDCAFASCTPGSTCI 354

RESULT 82
US-10-369-072-4
; Sequence 4, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerkhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
```

```
; APPLICANT: Szerkes, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-072-4

Query Match          55.0%; Score 66; DB 15; Length 1473;
Best Local Similarity 25.8%; Pred. No. 3.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

Oy 1 CXIXN----QXCXQLDDCCSXCNXXNXCVCV 27
Db 324 CVCVNGWGGDDCSENIDDCAFASCTPGSTCI 354

RESULT 83
US-10-322-281-726
; Sequence 726, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 726
; LENGTH: 2203
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-726

Query Match          55.0%; Score 66; DB 16; Length 2203;
Best Local Similarity 25.8%; Pred. No. 4.8e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

Oy 1 CXIXN----QXCXQLDDCCSXCNXXNXCVCV 27
Db 324 CVCVNGWGGDDCSENIDDCAFASCTPGSTCI 354
```

```
Db 78 CVCVNGWGGDDCSENIDDCAFASCTPGSTCI 108

RESULT 84
US-10-190-115-28
; Sequence 28, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezik, Amanda J.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 28
; LENGTH: 2447
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-28

Query Match          55.0%; Score 66; DB 15; Length 2447;
Best Local Similarity 29.0%; Pred. No. 5.3e+02;
Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps 1;

Oy 1 CXIXN----QXCXQLDDCCSXCNXXNXCVCV 27
Db 279 CVCVNGWGGDDCSENIDDCAFASCTPGSTCV 309
```

RESULT 85

US-10-369-072-28
; Sequence 28, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Groszke, William M
; APPLICANT: Szerkes, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigaru, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 28
; LENGTH: 2447
; TYPE: PRT
; ORGANISM: Takifugu rubripes

US-10-369-072-28

Query Match 55.0%; Score 66; DB 15; Length 2447;
Best Local Similarity 29.0%; Pred. No. 5.3e+02;
Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXCNXXNXCVCV 27

Db 279 CVCVNGWSGLDCSENIDDCDTAACSPGSTCV 309

RESULT 86

US-10-190-115-2
; Sequence 2, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.

; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szerkes, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Voss, Edward Z.

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/386,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 2
; LENGTH: 2469
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-190-115-2

Query Match 55.0%; Score 66; DB 15; Length 2469;
Best Local Similarity 25.8%; Pred. No. 5.3e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQXLDCCSXCNXXNXCVCV 27

Db 323 CVCVNGWSGDDCSENIDDCAFGACTPGSTCI 353

RESULT 87

US-10-369-072-2
; Sequence 2, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zerhusen, Bryan

RESULT 88
US-10-190-115-27
; Sequence 27, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grosse, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, "Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shimkets, Richard A.

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RESULT 89
US-10-369-072-27
/ Sequence 27, Application US/10369072
/ Publication No. US20040014081A1
/ GENERAL INFORMATION:
/ APPLICANT: Alsbrook II, John P
/ APPLICANT: Spaderna, Stephen K
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zerhusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Taupier, Raymond T
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Grosse, William M
/ APPLICANT: Szerkates, Edward S
/ APPLICANT: Lepley, Denise M
/ APPLICANT: Shen, Lei
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Shinkets, Richard
/ APPLICANT: Padigaru, Muralidhara
/ TITLE OF INVENTION: No. US20040014081
/ FILE REFERENCE: 21402-050 CON2

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; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 26
; LENGTH: 2317
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (440)..(440)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-10-190-115-26

Query Match          54.2%; Score 65; DB 15; Length 2317;
Best Local Similarity 30.0%; Pred. No. 6.2e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

Qy      1 CXIXN---QXCXQXLDCCSCXXCNXXNKC 26
Db      301 CVCVNGWTGSCSQNIDDCATAVCFHGATC 330

RESULT 100
US-10-369-072-26
; Sequence 26, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zernusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1e1 Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; PRIOR FILING DATE: 2003-02-18
; PRIOR APPLICATION NUMBER: 10/174,372
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
```

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; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2317
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (440)
; OTHER INFORMATION: Wherein Xaa represents O.
US-10-369-072-26
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Query Match          54.2%; Score 65; DB 15; Length 2317;
Best Local Similarity 30.0%; Pred. No. 6.2e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

Qy      1 CXIXN---QXCXQXLDCCSCXXCNXXNKC 26
Db      301 CVCVNGWTGSCSQNIDDCATAVCFHGATC 330

Search completed: April 18, 2005, 20:43:00
Job time : 93.5 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2005, 20:23:04 ; Search time 26.5 Seconds
(without alignments)
98.032 Million cell updates/sec

Title: US-10-627-685A-1

Perfect score: 120

Sequence: 1 CXIXNQXCQXLDDCCSXXCNXXNCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	27	2	kappa-conotoxin PV
2	77	64.2	26	2	omega-conotoxin MV
3	72	60.0	2524	2	Xotch protein - Af
4	69	57.5	29	2	omega-conotoxin MV
5	68	56.7	2555	2	notch protein homo
6	67	55.8	293	2	neurogenic repetit
7	67	55.8	2139	2	crumbs protein - f
8	67	55.8	2437	2	transmembrane prot
9	67	55.8	2531	2	notch protein homo
10	67	55.8	2531	2	notch-1 protein -
11	66	55.0	29	2	omega-conotoxin GV
12	66	55.0	1203	2	Motch B protein -
13	66	55.0	2471	2	cell-fate determin
14	66	55.0	2703	1	notch protein - fr
15	65	54.2	601	2	hypothetical prote
16	65	54.2	601	2	protein F40E10.4 [
17	65	54.2	1964	2	notch4 - mouse
18	65	54.2	2318	2	notch3 protein - h
19	65	54.2	2321	2	notch3 protein - se
20	65	54.2	2531	2	notch homolog
21	64	53.3	1372	2	hypothetical prote
22	64	53.3	2352	2	Notch homolog prot
23	64	53.3	3623	2	intrinsic factor-B
24	63	52.5	43	2	metallothionein -
25	63	52.5	570	2	fibropellin C prec
26	63	52.5	1687	2	EGF repeat transme
27	62	51.7	29	2	omega-conotoxin GV
28	62	51.7	722	2	DELTA-like 1 - mou
29	62	51.7	1064	2	fibropellin Ia - s

30	61.5	51.2	36	1	A32038	mu-agatoxin I - fu
31	61	50.8	29	2	A58537	omega-conotoxin MV
32	61	50.8	728	2	I50719	C-Delta-1 - chicke
33	61	50.8	1025	2	T42626	secreted leucine-r
34	61	50.8	1408	2	S16148	gene serrate prote
35	61	50.8	1469	2	B36655	slit protein 2 pre
36	61	50.8	1480	2	A36665	slit protein 1 pre
37	60	50.0	354	2	T22274	hypothetical prote
38	60	50.0	832	2	A31246	neurogenic protein
39	60	50.0	833	2	S19087	Gene Delta protein
40	60	50.0	880	2	S00670	neurogenic repetit
41	60	50.0	1225	2	A32901	glip protein precu
42	60	50.0	1722	2	B89753	protein FltC7.4 li
43	59	49.2	25	2	JH0701	omega-conotoxin MV
44	59	49.2	43	2	S33382	metallothionein -
45	59	49.2	43	2	S18173	metallothionein -
46	59	49.2	53	2	T10405	conotoxin-like pro
47	59	49.2	53	2	C72850	conotoxin homolog
48	59	49.2	53	2	T30499	conotoxin-like pro
49	59	49.2	63	2	A34958	metallothionein -
50	59	49.2	63	2	S33381	metallothionein -
51	59	49.2	63	2	A34620	metallothionein -
52	59	49.2	63	2	C34620	metallothionein -
53	59	49.2	419	2	T04215	hypothetical prote
54	59	49.2	1257	2	S28764	neurocan precursor
55	59	49.2	1268	2	S52781	neurocan - mouse
56	58.5	48.8	250	2	T16342	hypothetical prote
57	58.5	48.8	559	1	C9HU	complement C9 prec
58	58	48.3	63	2	S08191	metallothionein 2
59	58	48.3	387	2	B49175	Motch A protein -
60	58	48.3	861	2	A48825	Notch homolog Motc
61	58	48.3	3562	2	A47171	chondroitin sulfat
62	57	47.5	25	2	JH0700	omega-conotoxin MV
63	57	47.5	60	2	S31723	metallothionein -
64	57	47.5	1220	2	A56136	jagged protein pre
65	57	47.5	1531	2	T42218	slit-1 protein hom
66	56.5	47.1	217	2	S23244	hypothetical prote
67	56.5	47.1	1810	1	A32230	tenascin precursor
68	56	46.7	60	2	S38335	metallothionein -
69	56	46.7	68	2	S25775	testis-specific pr
70	56	46.7	164	2	T24272	hypothetical prote
71	56	46.7	188	2	H82933	hypothetical prote
72	56	46.7	188	2	T15651	hypothetical prote
73	56	46.7	198	2	T24476	hypothetical prote
74	56	46.7	385	2	S53718	homeotic protein d
75	56	46.7	385	2	A54785	preadipocyte facto
76	56	46.7	491	2	T21421	hypothetical prote
77	56	46.7	971	2	S23408	prematurely termin
78	56	46.7	1429	2	S06434	homeotic protein 1
79	56	46.7	1523	2	T13953	MEGF5 protein - ra
80	56	46.7	2610	2	T20968	hypothetical prote
81	55.5	46.2	121	1	PSSNAM	phospholipase A2 h
82	55.5	46.2	137	2	S68429	myotoxin precursor
83	55.5	46.2	571	2	T40996	conserved hypothet
84	55.5	46.2	613	2	S15468	complement C3b/C4b
85	55	45.8	118	2	T49515	hypothetical prote
86	55	45.8	152	2	S00332	alpha-amylase inhi
87	55	45.8	197	2	T46413	keratin KAP5.5 - s
88	55	45.8	383	2	S53716	delta-like homeoti
89	55	45.8	3623	2	T09456	intrinsic factor-B
90	54.5	45.4	42	1	NTIIRF	robustoxin - funne
91	54.5	45.4	42	1	NTIIV	versutoxin - funne
92	54.5	45.4	398	2	T39631	hypothetical prote
93	54.5	45.4	736	2	E71414	hypothetical prote
94	54.5	45.4	1046	2	A26838	praetalk protein p
95	54.5	45.4	1208	2	T27822	hypothetical prote
96	54.5	45.4	1766	2	A42135	trophozoite cystei
97	54.5	45.4	1959	1	AGRT	agrin - rat
98	54.5	45.4	2643	2	T29149	hypothetical prote
99	54	45.0	62	2	I51538	metallothionein -
100	54	45.0	67	2	T11547	metallothionein -


```

Query Match          57.5%; Score 69; DB 2; Length 29;
Best Local Similarity 30.8%; Pred. No. 2.5;
Matches      8; Conservative 12; Mismatches    6; Indels   0; Gaps    0;

Qy      1 CXIXNQXCXOXLDCCSXCNXXNKC 26
Db      3 CKKGAPCRKTMWDCCSGCGRRGKC 28
       | : : : : : ||| : : : : :
RESULT 5
A40043
notch protein homolog TAN-1 precursor - human
C:Species: Homo sapiens (man)
C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 16-Aug-2004
C:Accession: A40043
R:Eilissen, L.W.; Bird, J.; West, D.C.; Soreng, A.L.; Reynolds, T.C.; Smith, S.D.; Sklar,
Cell 66, 649-661, 1991
A>Title: TAN-1, the human homolog of the Drosophila Notch gene, is broken by chromosomal
A:Reference number: A40043; MUID:91347367; PMID:1831692
A:Accession: A40043
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-2555 <ELL>
A:Cross-references: GB:M73980
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:261-292/Domain: EGF homology <EGX1>
F:494-525/Domain: EGF homology <EGF1>
F:987-1018/Domain: EGF homology <EGX2>
F:1149-1180/Domain: EGF homology <EGF>
F:1187-1218/Domain: EGF homology <EGF3>
F:1233-1264/Domain: EGF homology <EGX3>
F:1237-1264/Domain: EGF homology <EGX3>
F:1237-1264/Domain: ankyrin repeat homology <AN1>
F:1960-1992/Domain: ankyrin repeat homology <AN2>
F:1994-2026/Domain: ankyrin repeat homology <AN3>
F:2027-2059/Domain: ankyrin repeat homology <AN4>
F:2060-2092/Domain: ankyrin repeat homology <AN5>

Query Match          56.7%; Score 68; DB 2; Length 2555;
Best Local Similarity 30.8%; Pred. No. 64;
Matches      8; Conservative 12; Mismatches    6; Indels   0; Gaps    0;

Qy      2 XIXNQXCXOXLDCCSXCNXXNKC 27
Db      248 GFTQGCEENIDCPGNCKNGGACV 273
       | : : : : : ||| : : : : :
RESULT 6
B26637
neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: B26637
R:Knust, E.; Dietrich, U.; Tepase, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-or
EMBO J. 6, 761-766, 1987
A>Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A:Reference number: A91081; MUID:87218537; PMID:3107986
A:Accession: B26637
A:Molecule type: mRNA
A:Residues: 1-293 <XNU>
A:Cross-references: UNIPROT:P10040; GB:X05144; NID:g7519; PIDN:CAA28793.1; PID:g929536
C:Genetics:
A:Gene: FlyBase:crb
A:Cross-references: FlyBase:FBgn0000368
C:Keywords: transmembrane protein
F:139-170/Domain: EGF homology <EGX1>
F:177-208/Domain: EGF homology <EGF1>
F:216-252/Domain: EGF homology <EGF>

Query Match          55.8%; Score 67; DB 2; Length 293;
Best Local Similarity 28.0%; Pred. No. 18;
Matches      7; Conservative 13; Mismatches    5; Indels   0; Gaps    0;

Qy      2 XIXNQXCXOXLDCCSXCNXXNKC 26

```

RESULT 9

S18188
Notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:g57634; PID:g57635
A:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF3>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 78;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXXCNXXKCV 27

DB 248 GFAGNCEENVDDCPGNCKNGGACV 273

RESULT 10

A46019
Notch-1 protein - mouse
A:Alternate names: notch protein
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: A46019; S25144; G49175; B46438; PHL569; S32109
R:del Amo, F.F.; Gendron-Maguire, M.; Swiatek, P.J.; Jenkins, N.A.; Copeland, N.G.; Grid
Genomics 15, 259-264, 1993
A:Title: Cloning, analysis, and chromosomal localization of Notch-1, a mouse homolog of
A:Reference number: A46019; MUID:93194170; PMID:8449489
A:Accession: A46019
A:Status: not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-2531
A:Cross-references: UNIPROT:Q01705; GB:Z11886; GB:S47228; NID:g288502; PIDN:CAA77941.1;
A:Note: sequence extracted from NCBI backbone (NCBIP:127318)
R:Franco del Amo, F.; Smith, D.E.; Swiatek, P.J.; Gendron-Maguire, M.; Greenspan, R.J.;
submitted to the EMBL Data Library, April 1992
A:Description: Expression pattern of Notch, a mouse homolog of Drosophila Notch, suggest
A:Reference number: S25144
A:Accession: S25144

A:Molecule type: mRNA
A:Residues: 1351-2108, 'Q', 2110-2114, 'ALP', 2118-2170 <PRA>
A:Cross-references: EMBL:Z11886
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B-two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1161-1547 <LAR>
A:Cross-references: EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287988
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126159)
R:Kopan, R.; Weintraub, H.
J. Cell Biol. 121, 631-641, 1993
A:Title: Mouse notch: expression in hair follicles correlates with cell fate determinati
A:Reference number: A46438; MUID:93252998; PMID:8486742

A:Accession: B46438

A:Status: preliminary

A:Molecule type: nucleic acid

A:Residues: 1865-1932, 'RR', 1935-1937, 'L', 1938-1967, 'I', 1969-2044, 'IE', 2047-2052, 'S', 2054-

A:Experimental source: embryo

A:Note: sequence extracted from NCBI backbone (NCBIN:131246, NCBIP:131247)

C:Comment: This protein has many EGF repeats and lin-12[1172]/Notch repeats.

C:Comment: This protein is one of the neurogenic proteins controlling the decision between

C:Genetics:

A:Gene: notch-1

A:Map position: 2

A:Note: proximal region of chromosome 2

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

F:106-138/Domain: EGF homology <EGF1>

F:144-175/Domain: EGF homology <EGF1>

F:222-254/Domain: EGF homology <EGF2>

F:261-292/Domain: EGF homology <EGF2>

F:339-370/Domain: EGF homology <EGF2>

F:416-449/Domain: EGF homology <EGF3>

F:456-487/Domain: EGF homology <EGF3>

F:494-525/Domain: EGF homology <EGF3>

F:532-563/Domain: EGF homology <EGF3>

F:607-638/Domain: EGF homology <EGF3>

F:682-713/Domain: EGF homology <EGF3>

F:757-788/Domain: EGF homology <EGF3>

F:795-826/Domain: EGF homology <EGF3>

F:873-904/Domain: EGF homology <EGF3>

F:911-942/Domain: EGF homology <EGF3>

F:949-980/Domain: EGF homology <EGF3>

F:987-1018/Domain: EGF homology <EGF3>

F:1025-1056/Domain: EGF homology <EGF3>

F:1063-1094/Domain: EGF homology <EGF3>

F:1149-1180/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGF3>

F:1233-1264/Domain: EGF homology <EGF3>

F:1352-1383/Domain: EGF homology <EGF3>

F:1391-1425/Domain: EGF homology <EGF3>

F:1917-1948/Domain: ankyrin repeat homology <AN1>

F:1949-1981/Domain: ankyrin repeat homology <AN2>

F:1983-2015/Domain: ankyrin repeat homology <AN3>

F:2016-2048/Domain: ankyrin repeat homology <AN4>

F:2049-2081/Domain: ankyrin repeat homology <AN5>

Query Match 55.8%; Score 67; DB 2; Length 2531;

Best Local Similarity 30.8%; Pred. No. 78;

Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXXCNXXKCV 27

DB 248 GFAGNCEENVDDCPGNCKNGGACV 273

RESULT 11

B43620

omega-conotoxin GVIIIB - cone shell (Conus geographus)

A:Alternate names: shaker peptide GVIIIB

C:Species: Conus geographus (geography cone)

C:Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: B43620

R:Oliviera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santos

Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: B43620

A:Molecule type: protein

A:Residues: 1-29 <OLI>

A:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydroxyproline;

F:1-16, 8-19, 15-26/Diulfide bonds: #status predicted

F:4, 7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 55.0%; Score 66; DB 2; Length 29;

Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXXCNXXNXC 27
Db 822 TGQKCTNIDCVTPNGNGGTCTI 845

RESULT 15
T22025
hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22025
R:Smyle, R.
submitted to the EMBL Data Library, February 1996
A:Reference number: Z19503
A:Accession: T22025
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-601 <WIL>
A:Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10
A:Experimental source: clone F40E10
C:Genetics:
A:Gene: CESP:F40E10.4
A:Map position: X

Query Match 54.2%; Score 65; DB 2; Length 601;
Best Local Similarity 26.9%; Pred. No. 46;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXLDCCSXXCNXXNXC 27
Db 114 GFEGDYCEKNIDCVNSKENGKVC 139

RESULT 16
D89711
Protein F40E10.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89711
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 287, 122, 1999
A:Accession: D89711
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-601 <STO>
A:Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
C:Genetics:
A:Gene: F40E10.4
A:Map position: X

Query Match 54.2%; Score 65; DB 2; Length 601;
Best Local Similarity 26.9%; Pred. No. 46;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXLDCCSXXCNXXNXC 27
Db 114 GFEGDYCEKNIDCVNSKENGKVC 139

RESULT 17
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; and others
submitted to the EMBL Data Library, October 1997

A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:G2564945; PID:G2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 671/1; 1679/3; 1729/1; 1761/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>

Query Match 54.2%; Score 65; DB 2; Length 1964;
Best Local Similarity 33.3%; Pred. No. 1e+02;
Matches 7; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

QY 7 XCXQXLDCCSXXCNXXNXC 27
Db 348 GCEENLDDCAATCAPGSTCI 368

RESULT 18
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 46, 123-136, 1994
A>Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-like repeats
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:G483580; PIDN:CAA52776.1; PID:G483580
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:474-505/Domain: EGF homology <EGF>
F:854-885/Domain: EGF homology <EGF2>
F:1839-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1939-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 54.2%; Score 65; DB 2; Length 2318;
Best Local Similarity 30.0%; Pred. No. 1.1e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

QY 1 CXIXN-----QXCXQXLDCCSXXCNXXNXC 26
Db 301 CVCVNGWTGSCSQNIDCATAVCFHGATC 330

RESULT 19
S78549
notch3 protein - human
C:Species: Homo sapiens (man)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S78549; S71825
R:Joutel, A.; Tournier-Lasserre, E.
submitted to the EMBL Data Library, April 1997
A:Reference number: S78549
A:Accession: S78549
A:Molecule type: mRNA
A:Residues: 1-2321 <JOUT1>
A:Cross-references: UNIPROT:Q9UM47; EMBL:U97669; NID:G2668591; PIDN:AA891371.1; PID:G2668591
R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrier, H.; Mouton, P.; Alamowitch

DB 205 GFTGDCNCETDIDECASAPCRNGGACV 230

RESULT 26

T30176

ECF repeat transmembrane protein - mouse

C:Species: Mus musculus (house mouse)

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30176

R:Sell, C.; Hoff III, H.B.

A:Submitted to the EMBL Data Library, May 1996

A:Description: Cloning of a novel mRNA regulated by the insulin like growth

A:Reference number: Z20762

A:Accession: T30176

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-1687 <SEL>

A:Cross-references: UNIPROT:G61204; EMBL:U57368; NID:gl336627; PID:gl336628

A:Experimental source: strain C57BL/6J; clone DBI-1; whole embryo

Query Match 52.5%; Score 63; DB 2; Length 1687;

Best Local Similarity 26.9%; Pred No. 1.4e+02;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps

QY 2 XIXNQXCXQXLDCCSXCNXXNXCVCV 27

DB 480 GFEGSTCERNIDDCPNHRCQNGVCV 505

RESULT 27

A43620

omega-conotoxin GVIIA - cone shell (Conus geographus)

N:Alternate names: shaker peptide GVIIA

C:Species: Conus geographus (geography cone)

C>Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004

C:Accession: A43620

R:Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, Science 230, 1338-1343, 1985

A:Title: Peptide neurotoxins from fish-hunting cone snails.

A:Reference number: A43620; MUID:86070213; PMID:4071055

A:Accession: A43620

A:Molecule type: protein

A:Residues: 1-29 <OLI>

A:Cross-references: UNIPROT:P05483

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; calcium channel inhibitor; hydro; 1-16,18,19,15-26/disulfide bonds; #status predicted

F;4,7/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 51.7%; Score 62; DB 2; Length 29;

Best Local Similarity 26.9%; Pred No. 11;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps

QY 1 CXIXNQXCXQXLDCCSXCNXXNXC 26

DB 1 CKSPGTCGRMRDCTCSLLYSNKC 26

RESULT 28

I48324

DETA-like 1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48324

R:Bettenhausen, B.; de Angelis, M.H.; Simon, D.; Guenet, J.L.; Gossler, A. Development 121, 2407-2418, 1995

A:Title: Transient and restricted expression during mouse embryogenesis of

A:Reference number: I48324; MUID:95401858; PMID:7671806

A:Accession: I48324

A:Status: preliminary;

A:Molecule type: mRNA

A:Residues: 1-722 <RES>

A:Cross-references: UNIPROT:O61483; EMBL:Y80903; NID:G906569; PID:G906569

Query Match	50.8%;	Score 61;	DB 2;	Length 1480;
Best Local Similarity	26.9%;	Pred. No. 26+02;		
Matches	7;	Conservative 12;	Mismatches 7;	Indels 0;
F;125-148/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT2>				
F;149-172/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT3>				
F;173-196/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT4>				
F;197-220/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT5>				
F;228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>				
F;288-313/Domain: proteoglycan amino-terminal homology <PAH2>				
F;323-346/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT6>				
F;347-370/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT7>				
F;371-394/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT8>				
F;395-418/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT9>				
F;419-442/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT10>				
F;450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>				
F;512-537/Domain: proteoglycan amino-terminal homology <PAH3>				
F;547-571/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT11>				
F;572-595/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT12>				
F;596-619/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT13>				
F;620-643/Domain: proteoglycan carboxyl-terminal homology <PCS3>				
F;651-695/Domain: proteoglycan amino-terminal homology <PAH4>				
F;708-733/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT15>				
F;743-766/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT16>				
F;767-790/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT17>				
F;791-814/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT18>				
F;815-838/Domain: lucine-rich alpha-2-glycoprotein repeat homology <LRRT19>				
F;846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>				
F;1028-1061/Domain: EGF homology <EGF>				
F;1068-1099/Domain: EGF homology <EGF2>				
F;1115-1148/Domain: EGF homology <EGF1>				

1055 GFHGTCTDNIDDCQNHMCQGGTCV 1080

RESULT 37
T22274
hypothetical protein F46B3.9 - *Caenorhabditis elegans*

C;Accession: T22274
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19541
A;Accession: T22274
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-354 <WIL>
A;Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN
A;Experimental source: clone F46B3
C;Genetics:
A;Gene: CESP:F46B3.9
A;Map position: 5
A;Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1

Query Match 50.0%; Score 60; DB 2; Length 354;
Best Local Similarity 28.6%; Pred. No. 94;
Matches 8; Conservative 13; Mismatches 5; Indels 2; Gaps

```
QY      1 CIXN--QXCXKLDCCSXCNXXNC 26
        |||::|||::|::|
        |::|::|::|::|
Db     158 CKLVNGPKVPELDCSHIKCSIGSHC 185

RESULT 38
A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2000
R:Accession: A31246
R:Kopczyński, C.C.; Alton, A.K.; Fechtel, K.; Koob, P.J.; Muskavitch, M.A.
```

Genes Dev. 2, 1723-1735, 1988
A;Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a
A;Reference number: A31246; MUID:89196890; PMID:3149249
A;Accession: A31246
A;Molecule type: mRNA
A;Residues: 1-832 <KOP>
A;Cross-references: GB:Y00222
C;Genetics:
A;Gene: FlyBase:DL
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;295-328/Domain: EGF homology <EGX1>
F;422-450/Domain: EGF homology <EGF1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
Query Match 50.0%; Score 60; DB 2; Length 832;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNOXCXOXLDCCSXXCNXXNXCXV 27
DB 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 39
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S19087
R;Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A;Reference number: S19087
A;Accession: S19087
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-833 <MUS>
A;Cross-references: UNIPROT:P10041; EMBL:Y00222
C;Genetics:
A;Gene: FlyBase:DL
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
F;335-371/Domain: EGF homology <EGF1>
F;378-415/Domain: EGF homology <EGX1>
F;457-488/Domain: EGF homology <EGF>
F;533-564/Domain: EGF homology <EGF3>
Query Match 50.0%; Score 60; DB 2; Length 833;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNOXCXOXLDCCSXXCNXXNXCXV 27
DB 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 40
S00670
neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: gene DL protein
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: S00670; A26637
R;Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
EMBO J. 6, 3431-3440, 1987
A;Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A;Reference number: S00670
A;Accession: S00670
A;Molecule type: mRNA
A;Residues: 1-880 <VAE>
A;Cross-references: UNIPROT:P10041; EMBL:X06289; NID:g7852; PID:g7853
R;Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega

EMBO J. 6, 761-766, 1987
A;Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A;Reference number: A91081; MUID:87218537; PMID:3107986
A;Accession: A26637
A;Molecule type: mRNA
A;Residues: 422-436, 'ET', 439-458, 'A', 460-489, 'T', 491-621 <KNU>
A;Cross-references: GB:X05140; NID:g7851; PIDN:CAA28786.1; PID:g929563
C;Genetics:
A;Gene: Delta; DL
A;Cross-references: FlyBase:FBgn0000463
C;Superfamily: neurogenic protein delta; EGF homology
C;Keywords: transmembrane protein
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F;457-488/Domain: EGF homology <EGF1>
F;533-564/Domain: EGF homology <EGF2>
Query Match 50.0%; Score 60; DB 2; Length 880;
Best Local Similarity 23.1%; Pred. No. 1.7e+02;
Matches 6; Conservative 12; Mismatches 8; Indels 0; Gaps 0;
QY 2 XIXNOXCXOXLDCCSXXCNXXNXCXV 27
DB 444 GFSGTRCETNIDDLGHQCENGGTCTI 469
RESULT 41
A32901
glp1 protein precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Dec-1989 #sequence_revision 04-Sep-1992 #text_change 09-Jul-2004
C;Accession: A32901
R;Jochem, J.; Greenwald, I.
Cell 58, 553-563, 1989
A;Title: glp-1 and lin-12, genes implicated in distinct cell-cell interactions in Caenorhabditis
A;Reference number: A32901; MUID:89336787; PMID:2758466
A;Accession: A32901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1295 <YOC>
A;Cross-references: UNIPROT:P13508; GB:M25580; NID:g156316; PIDN:AAA28058.1; PID:g156317
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;121-151/Domain: EGF homology <EGF1>
F;275-307/Domain: EGF homology <EGX1>
F;373-405/Domain: EGF homology <EGF>
F;411-442/Domain: EGF homology <EGF3>
F;450-478/Domain: EGF homology <EGF2>
F;961-993/Domain: ankyrin repeat homology <AN1>
F;1074-1106/Domain: ankyrin repeat homology <AN2>
F;1107-1139/Domain: ankyrin repeat homology <AN3>
Query Match 50.0%; Score 60; DB 2; Length 1295;
Best Local Similarity 25.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 13; Mismatches 6; Indels 4; Gaps 1;
QY 1 CXIXN---QXCXOXLDCCSXXCNXXNXCXV 27
DB 140 CICNNGYGGSYCEGIDHCAQNECAEGSTCV 170
RESULT 42
E89753
protein Fl1C7.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89753
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXIXNQXQXLDDCCSXXCNXXNC 26
| : | : | : | : | : | : | :
Db 6 CKKXNCRSCRKSCCSCPAGCNC 31

RESULT 45
S18173
metallothionein - common bobwhite (fragment)
C:Species: Colinus virginianus (Common bobwhite)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33378; S18173
R:Shartzel, K.L.; Kage, K.; Sobieski, R.J.; Andrews, G.K.
J. Mol. Evol. 36, 255-262, 1993
A:Title: Evolution of avian metallothionein: DNA sequence analyses of the turkey metallo
A:Reference number: S33378; MUID:93247066; PMID:8483164
A:Accession: S33378
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-43 <SHA>
A:CROSS-references: UNIPROT:P27086; EMBL:XG2511; NID:g62749; PIDN:CAA44370.1; PID:g62750
C:Superfamily: metallothionein

Query Match 49.2%; Score 59; DB 2; Length 43;
Best Local Similarity 30.8%; Pred. No. 28;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXIXNQXQXLDDCCSXXCNXXNC 26
| : | : | : | : | : | : | :
Db 6 CKKXNCRSCRKSCCSCPAGCNC 31

A:Title: The sequence of the Orygia pseudotsugata multinnucleocapsid nuclear polyhedrosis virus
A:Reference number: Z17011; MUID:97271300; PMID:9126251
A:Accession: T10405
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-53 <NR>
A:CROSS-references: EMBL:U75930; NID:g2934903; PID:g1911382

Query Match 49.2%; Score 59; DB 2; Length 53;
Best Local Similarity 32.1%; Pred. No. 32;
Matches 9; Conservative 13; Mismatches 4; Indels 2; Gaps 2;

Qy 1 CXIXNQXQXLDDCCSXXCN-XXNXCV 27
| : | : | : | : | : | : | :
Db 25 CAETGAVCHS-DECCSGACSPFNYCL 51

RESULT 47
C72850
conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, ACMPV
A:Note: dsDNA virus
C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C:Accession: C72850; A44003
R:Ayres, M.D.; Howard, S.C.; Kusio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A:Reference number: A72850; MUID:94303173; PMID:8030224
A:Accession: C72850
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-53 <AYR>

A;Residues: 1-63 <LIN>
A;Cross-references: UNIPROT:P09576
A;Experimental source: Anas platyrhynchos (domestic duck)
A;Accession: B34620

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-63 <L12>

A;Experimental source: Anas platyrhynchos x Cairina moschata (domestic duck x muscovy duck)
R;Lin, L.Y.; Liu, L.F.; Tam, M.F.; Huang, P.C.; Vestling, M.; Fenselau, C.
Biochim. Biophys. Acta 1041, 31-35, 1990

A;Title: Primary sequence of duck metallothionein.

A;Reference number: S13154; MUID:91027866; PMID:2223844

A;Accession: S13154

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-63 <L13>

R;Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.

Gene 176, 85-92, 1996

A;Title: Structure and expression of metallothionein gene in ducks.

A;Reference number: JC5094; MUID:97075914; PMID:8918237

A;Accession: JC5095

A;Molecule type: mRNA

A;Residues: 1-63 <LEE>

A;Cross-references: GB:U34231; NID:g1000299; PIDN:AAC60048.1; PID:g1000300

A;Experimental source: Strain tsai ya duck

C;Comment: This protein has a high metal binding capacity and sulfur content.

C;Genetics:

A;Gene: mt

A;Introns: 11/1; 33/1

C;Superfamily: metallothionein

Query Match 49.2%; Score 59; DB 2; Length 63;

Best Local Similarity 30.8%; Pred. No. 36;

Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNC 26

DB 20 CKCKNCRSCRKSCCSCCPAGCNC 45

RESULT 52

C34620

metallothionein - muscovy duck

C;Species: Cairina moschata (muscovy duck)

C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004

C;Accession: C34620; JC5094

R;Lin, L.Y.; Huang, P.C.

Biochem. Biophys. Res. Commun. 168, 182-187, 1990

A;Title: Complete homology in metallothionein from two genera of ducks and their hybrids

A;Reference number: A34620; MUID:90226357; PMID:2327997

A;Accession: C34620

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-63 <LIN>

A;Cross-references: UNIPROT:P09576

R;Lee, Y.J.; Chen, Y.P.; Wang, S.H.; Chow, W.Y.; Lin, L.Y.

Gene 176, 85-92, 1996

A;Title: Structure and expression of metallothionein gene in ducks.

A;Reference number: JC5094; MUID:97075914; PMID:8918237

A;Accession: JC5094

A;Molecule type: mRNA

A;Residues: 1-63 <LEE>

A;Cross-references: GB:U34230; NID:g1000297; PIDN:AAC60047.1; PID:g1000298

C;Comment: This protein has a high metal binding capacity and sulfur content.

C;Genetics:

A;Gene: mt

A;Introns: 11/1; 33/1

C;Superfamily: metallothionein

Query Match 49.2%; Score 59; DB 2; Length 63;

Best Local Similarity 30.8%; Pred. No. 36;

Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNC 26

DB 20 CKCKNCRSCRKSCCSCCPAGCNC 45

RESULT 53

T04215

hypothetical protein T5C23.110 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C;Accession: T04215

R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,

submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15261

A;Accession: T04215

A;Molecule type: DNA

A;Residues: 1-419 <BEV>

A;Cross-references: UNIPROT:Q9T0D5; EMBL:AL049500

A;Experimental source: cultivar Columbia; BAC clone T5C23

C;Genetics:

A;Map position: 4

A;Introns: 200/2; 241/2; 285/3

A;Note: T5C23.110

Query Match 49.2%; Score 59; DB 2; Length 419;

Best Local Similarity 28.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNOXCXQXLDCCSXCNXXNC 25

DB 353 CKIDNAWLMILQECICUCYEYDG 377

RESULT 54

S28764

neurocan precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S28764

R;Rauch, U.; Karthikeyan, L.; Maurel, P.; Margolis, R.K.

J. Biol. Chem. 267, 19536-19547, 1992

A;Title: Cloning and primary structure of neurocan, a developmentally regulated, aggregat

A;Reference number: S28764; MUID:92406907; PMID:1326557

A;Accession: S28764

A;Molecule type: mRNA

A;Residues: 1-1257 <RAU>

A;Cross-references: UNIPROT:P55067; EMBL:M97161; NID:g205649; PIDN:AAC37679.1; PID:g20561

C;Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; BG

C;Keywords: chondroitin sulfate proteoglycan; glycoprotein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-1257/Product: neurocan #status predicted <MAT>

F;176-253/Domain: link protein repeat homology <LNK1>

F;274-355/Domain: link protein repeat homology <LNK2>

F;364-366/Region: cell attachment (R-G-D) motif

F;953-984/Domain: EGF homology <EGF>

F;1029-1149/Domain: C-type lectin homology <LCH>

F;1156-1212/Domain: complement factor H repeat homology <FHD>

F;121,339,737,967,1164/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;372,410/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

F;944/Binding site: chondroitin sulfate (Ser) (covalent) #status experimental

Query Match 49.2%; Score 59; DB 2; Length 1257;

Best Local Similarity 25.0%; Pred. No. 2.7e+02;

Matches 6; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNOXCXQXLDCCSXCNXXNCV 27

DB 980 AGENCEIDDCLCSPCENGTCI 1003

RESULT 55

SS2781

neurocan - mouse

C:Species: Mus musculus (house mouse)
 C>Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S52781
 R:Rauch, U.; Forsberg, N.; Kulbe, G.; Arnold-Ammer, I.; Faessler, R.
 submitted to the EMBL Data Library, February 1995
 A:Description: Amino acid sequence of mouse neurocan and brevican and their different ex
 A:Reference number: S52781
 A:Accession: S52781
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1268 <RAU>
 A:CROSS-references: UNIPROT:P55066; EMBL:X84727; NID:G758629; PIDN:CAA59216.1; PID:G7586
 C:Superfamily: aggrecan; C-type lectin homology; complement factor H repeat homology; EG
 F:176-253/Domain: link protein repeat homology <LNK1>
 F:274-355/Domain: link protein repeat homology <LNK2>
 F:964-995/Domain: EGF homology <EGF>
 F:1040-1160/Domain: C-type lectin homology <LCH>
 F:1167-1223/Domain: complement factor H repeat homology <FHD>
 Query Match 49.2%; Score 59; DB 2; Length 1268;
 Best Local Similarity 25.0%; Pred. No. 2.7e+02;
 Matches 6; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 Qy 4 XNQXCXQXLDCCSXKCNXXKCV 27
 Db 991 AGENCEIDIDCLCSPCENGTCI 1014
 RESULT 56
 T16342
 hypothetical protein F42C5.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16342
 R:Du, Z.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid F42C5.
 A:Reference number: T16342
 A:Accession: T16342
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-250 <DUZ>
 A:CROSS-references: UNIPROT:Q20327; EMBL:U40799; NID:G1065935; PID:G1065941; PIDN:AAA814
 C:Genetics:
 A:Gene: CESP:F42C5.7
 A:Introns: 15/2; 40/3; 167/3; 191/3
 Query Match 48.8%; Score 58.5; DB 2; Length 250;
 Best Local Similarity 32.0%; Pred. No. 1e+02;
 Matches 8; Conservative 11; Mismatches 3; Indels 3; Gaps 1;
 Qy 2 XIXNQXCXQXLDCCSXKCNXXKCV 26
 Db 134 PVFNQYAMOPANDCC---CRCGSPC 155
 RESULT 57
 C9HU
 complement C9 precursor [validated] - human
 C:Species: Homo sapiens (man)
 C>Date: 27-Nov-1985 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
 C:Accession: A59363; I52400; A91029; S68647; A59364; A03208
 R:Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
 unpublished results, 1988, cited by GenBank
 A:Description: Relationships between the gene and protein structure in human complement
 A:Reference number: A59363
 A:Accession: A59363
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-559 <WARI>
 A:CROSS-references: UNIPROT:P02748; GB:X02176; NID:G29580; PIDN:CAA26117.1; PID:G29581
 R:Maraziti, D.; Eggertsen, G.; Fey, G.H.; Stanley, K.K.
 Biochemistry 27, 6529-6534, 1988

A:Title: Relationships between the gene and protein structure in human complement compone
 A:Reference number: I52400; MUID:89118250; PMID:3219351
 A:Accession: I52400
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 62-159 <WARI>
 A:CROSS-references: GB:J02833; NID:G179727; PIDN:AAA51890.1; PID:G179728
 R:Stanley, K.K.; Kocher, H.P.; Luzio, J.P.; Jackson, P.; Tschopp, J.
 EMBO J. 4, 375-382, 1985
 A:Title: The sequence and topology of human complement component C9.
 A:Reference number: A91029; MUID:85257464; PMID:4018030
 A:Accession: A91029
 A:Molecule type: mRNA
 A:Residues: S'1-313,315-559 <STA>
 A:CROSS-references: GB:X02176; NID:G29580
 R:DiScipio, R.G.; Gehring, M.R.; Podack, E.R.; Kan, C.C.; Hugli, T.E.; Fey, G.H.
 Proc. Natl. Acad. Sci. U.S.A. 81, 7298-7302, 1984
 A:Title: Nucleotide sequence of cDNA and derived amino acid sequence of human complement
 A:Reference number: A94019; MUID:85063778; PMID:6095282
 A:Accession: A94019
 A:Molecule type: mRNA
 A:Residues: 2-12,'X',14-16,'X',18-42,'R',44-313,315-416,'P',418-559 <DIS>
 A:CROSS-references: GB:K02766; NID:G179725; PIDN:AAA51889.1; PID:G179726
 R:Lengweiller, S.; Schaller, J.; Rickli, E.E.
 FEBS Lett. 380, 8-12, 1995
 A:Title: Identification of disulfide bonds in the ninth component (C9) of human complement
 A:Reference number: S68647; MUID:96181657; PMID:8603752
 A:Accession: S68647
 A:Molecule type: protein
 A:Residues: 34-47;52-59;69-87,'X',89-93,'T',94-98;106-113;118-131;136-145;180-181,'X',182
 R:Witze-Schlomp, K.; Hobart, M.J.; Fernie, B.A.; Orren, A.; Wurzman, R.; Rittner, C.; Kau
 Immunogenetics 48, 144-147, 1998
 A:Title: Heterogeneity in the genetic basis of human complement C9 deficiency.
 A:Reference number: A59364; MUID:98298010; PMID:9634479
 A>Note: submitted to GenBank, September 1996
 A:Accession: A59364
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 27-559 <WIT>
 A:CROSS-references: GB:Y08545; NID:G1834472; PIDN:CAA69849.1; PID:G2258128
 A:Experimental source: macronuclear; tissue type blood; cell type lymphocyte
 R:Horstenger, J.; Blommestein, M.; Hess, D.; Furmanek, A.; Miroshnichenko, O.
 J. Biol. Chem. 274, 32786-32794, 1999
 A:Title: The four terminal components of the complement system are C-mannosylated on mult
 A:Reference number: A59362; MUID:20020247; PMID:10551839
 A:Contents: annotation
 A>Note: identification and location of C-mannosylation sites by mass-spectroscopy and (1)
 C:Genetics:
 A:Gene: GDB:C9
 A:CROSS-references: GDB:119738; OMIM:120940
 A:Map position: 5p13-5p13
 C:Complex: monomer in plasma; 10 to 16 chain multimer in transmembrane form
 C:Function:
 A:Description: in association with complement C5b-8 complex polymerizes to form a transme
 A:Pathway: complement pathway
 C:Superfamily: complement C9; EGF homology; LDL receptor ligand-binding repeat homology;
 C:Keywords: complement pathway; cytolysis; glycoprotein; inflammation; membrane attack c
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-265,266-559/Product: complement C9 #status predicted <MAT>
 F:22-265/Domain: complement C9a #status predicted <C9A>
 F:41-95/Domain: thrombospondin type 1 repeat homology <THR>
 F:101-134/Domain: LDL receptor ligand-binding repeat homology <LDL>
 F:266-559/Domain: complement C9b #status predicted <C9B>
 F:510-539/Domain: EGF homology <EGF>
 F:43-78,54-57,88-94,142-181,254-255,380-405,510-526,513-528,530-539/Disulfide bonds: #ste
 F:48/Modified site: 2'-mannosyl-tryptophan (Trp) #status experimental
 F:51/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental
 F:265-266/Cleavage site: His-Gly (thrombin) #status predicted
 F:277,415/Binding site: carbohydrate (Asn) #status predicted
 Query Match 48.8%; Score 58.5; DB 1; Length 559;
 Best Local Similarity 26.3%; Pred. No. 1.8e+02;
 Matches 10; Conservative 12; Mismatches 3; Indels 13; Gaps 2;

```
QY 2 XINQXQXQXLDG-----CS-----XXCNXXNXC 26
   : : : : : ||| ||| : : : : :
Db 88 CVTEPCDAEDDCGDFQCGTCIKWRLRCNGDNC 125

RESULT 58
S08191
metallothionein 2 - pigeon
C:Species: Columba livia (domestic pigeon)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S08191
R:Lin, L.Y.; Lin, W.C.; Huang, P.C.
Biochim. Biophys. Acta 1037, 248-255, 1990
A:Title: Pigeon metallothionein consists of two species.
A:Reference number: S08190; MUID:90167121; PMID:2407296
A:Accession: S08191
A:Molecule type: protein
A:Residues: 1-63 <LIN>
A:Cross-references: UNIPROT:P15787
C:Superfamily: metallothionein
C:Keywords: blocked amino end
F:1/Modified site: blocked amino end (Met) (probably acetylated) #status experimental

Query Match 48.3%; Score 58; DB 2; Length 63;
Best Local Similarity 32.3%; Pred. No. 45;
Matches 10; Conservative 11; Mismatches 6; Indels 4; Gaps 2;

QY 1 CXTXN--QXCXQLDDCCSXXC-NXXNXC 27
   : : : : : ||| ||| : : : : :
Db 20 CKCNCRQSCRKSCCSCCPASCNCAKGC 50

RESULT 59
B49175
Morch A protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: Mus musculus (house mouse)
C>Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: B49175; PFI569; S32109
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of tissues.
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: B49175
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-387 <LAR>
A:Cross-references: UNIPROT:Q01705; EMBL:X68278; NID:g287987; PIDN:CAA48339.1; PID:g287987
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126159)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:27-58/Domain: EGF homology <EGF>
F:73-104/Domain: EGF homology <EGF2>
F:151-185/Domain: EGF homology <EGF1>

Query Match 48.3%; Score 58; DB 2; Length 387;
Best Local Similarity 20.8%; Pred. No. 1.5e+02;
Matches 5; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNOXCXQXLDCCSXXCXCNXXNXC 27
   : : : : : ||| ||| : : : : :
Db 16 HGSNCSEINECLSQPCQNGTCTI 39

RESULT 60
A48825
Notch homolog Notch protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C:Accession: A48825
```

```
R;Reaume, A.G.; Conlon, R.A.; Zirngibl, R.; Yamaguchi, T.P.; Rossant, J.
Dev. Biol. 154, 377-387, 1992
A:Title: Expression analysis of a Notch homologue in the mouse embryo.
A:Reference number: A48825; MUID:93050801; PMID:1426644
A:Accession: A48825
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-861 <REA>
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:119144)
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology
F:26-57/Domain: EGF homology <EGF>
F:64-95/Domain: EGF homology <EGX1>
F:198-229/Domain: EGF homology <EGF2>
F:441-472/Domain: EGF homology <EGX2>

Query Match 48.3%; Score 58; DB 2; Length 861;
Best Local Similarity 20.8%; Pred. No. 2.6e+02;
Matches 5; Conservative 14; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNOXCXQXLDCCSXXCXCNXXNXC 27
   : : : : : ||| ||| : : : : :
Db 384 HGSNCSEINECLSQPCQNGTCTI 407

RESULT 61
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken
C:Species: Gallus gallus (chicken)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A47171
R;Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A:Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during embryonic development.
A:Reference number: A47171; MUID:93300846; PMID:8314802
A:Accession: A47171
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-3562 <SHI>
A:Cross-references: UNIPROT:O90953; GB:D13542; NID:G391643; PIDN:BAA02742.1; PID:G391644
A:Experimental source: stage 22-23 developing limb buds
A:Note: sequence extracted from NCBI backbone (NCBIP:134456; NCBIP:134457)
C:Superfamily: chicken chondroitin sulfate proteoglycan PG-M core protein; C-type lectin
F:166-243/Domain: link protein repeat homology <LNK1>
F:264-345/Domain: link protein repeat homology <LNK2>
F:3258-3289/Domain: EGF homology <EGF1>
F:3296-3327/Domain: EGF homology <EGF>
F:3334-3454/Domain: C-type lectin homology <LCH>
F:3461-3517/Domain: complement factor H repeat homology <FHD>

Query Match 48.3%; Score 58; DB 2; Length 3562;
Best Local Similarity 23.1%; Pred. No. 6.8e+02;
Matches 6; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXQXLDCCSXXCXCNXXNXC 27
   : : : : : ||| ||| : : : : :
Db 3283 GFNGEQCELDIDECQSNPCRGATCI 3308

RESULT 62
JH0700
omega-conotoxin MVIIA [validated] - cone shell (Conus magus)
C:Species: Conus magus (magus cone)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: JH0700; C60133; A34115
R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M.
Neuron 9, 69-77, 1992
A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A:Reference number: JH0699; MUID:92337922; PMID:1352986
A:Accession: JH0700
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
```

A;Residues: 1-25 <HIL>
A;Cross-references: UNIPROT:P05484
R;Olivera, B.M.; Gray, W.R.; Zeikus, R.; McIntosh, J.M.; Varga, J.; Rivier, J.; de Santis, Science 230, 1338-1343, 1985
A;Title: Peptide neurotoxins from fish-hunting cone snails.
A;Reference number: A43620; MUID:86070213; PMID:4071055
A;Accession: C60133
A;Molecule type: protein
A;Residues: 1-25 <OLI>
R;Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.; Biochemistry 26, 2086-2090, 1987
A;Title: Neuronal calcium channel antagonists. Discrimination between calcium channel subtypes.
A;Reference number: A34115; MUID:87299637; PMID:2441741
A;Contents: annotation
R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Reference number: A67648; PDB:1MWI
A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
R;Nielsen, K.J.; Thomas, L.; Lewis, R.J.; Alewood, P.F.; Craik, D.J.
J. Mol. Biol. 263, 297-310, 1996
A;Title: A consensus structure for omega-conotoxins with different selectivities for voltage-gated calcium channels.
A;Reference number: A58619; MUID:97070382; PMID:8913308
A;Contents: annotation; conformation by (1)H-NMR
R;Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.
submitted to the Brookhaven Protein Data Bank, April 1995
A;Reference number: A66296; PDB:1QMG
A;Contents: annotation; conformation by (1)H-NMR, residues 1-25
R;Kohn, T.; Kim, J.I.; Kobayashi, K.; Koder, Y.; Maeda, T.; Sato, K.
Biochemistry 34, 10256-10265, 1995
A;Title: Three-dimensional structure in solution of the calcium channel blocker omega-conotoxin MVIIA.
A;Reference number: A58627; MUID:95367555; PMID:7640281
A;Contents: annotation; conformation by (1)H-NMR
C;Superfamily: omega-conotoxin
C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inhibitor; 1-16, 8-20, 15-25/Disulfide bonds: #status predicted
F;1-16, 8-20, 15-25/Disulfide bonds: #status predicted
F;25/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 47.5%; Score 57; DB 2; Length 25;
Best Local Similarity 24.0%; Pred. No. 30;
Matches 6; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXQXQLDDCCSXCNXXNX 25
DB 1 CKGKAKSLMYDCTGTGCRSGKC 25

RESULT 63
S31723
Metallothionein - northern pike
C;Species: Esox lucius (northern pike)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S38334; S17175; S15503; S31723
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish.
A;Reference number: S38334; MUID:94032489; PMID:8218416
A;Accession: S38334
A;Molecule type: DNA
A;Residues: 1-60 <KIL>
A;Cross-references: UNIPROT:P25127; EMBL:X70042; NID:G62782; PIDN:CAA49636.1; PID:G62783
A;Note: the authors translated the codon ACT for residue 9 as Ser
R;Kille, P.; Stephens, P.E.; Kay, J.
Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach, and goldfish.
A;Reference number: S16996; MUID:91316146; PMID:1859844
A;Accession: S17175
A;Molecule type: mRNA
A;Residues: 1-60 <KIL>
A;Cross-references: EMBL:X59392; NID:G62780; PIDN:CAA42035.1; PID:G62781
C;Genetics:
A;Introns: 9/1, 31/1
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 47.5%; Score 57; DB 2; Length 60;
Best Local Similarity 26.9%; Pred. No. 54;
Matches 7; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 CXIXNQXQXQLDDCCSXCNXXNX 26
DB 18 CKSCNCACTSCCKSCGCGPSCGSKC 43

RESULT 64
A56136
Jagged protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 21-Jul-2003
C;Accession: A56136
R;Lindseil, C.E.; Shawber, C.J.; Boulter, J.; Weinmaster, G.
Cell 80, 909-917, 1995
A;Title: Jagged: a mammalian ligand that activates Notch1.
A;Reference number: A56136; MUID:95211842; PMID:7697721
A;Accession: A56136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1220 <LIN>
A;Cross-references: GB:L38483
F;379-410/Domain: EGF homology <EGF1>
F;492-523/Domain: EGF homology <EGF>
F;634-665/Domain: EGF homology <EGF2>

Query Match 47.5%; Score 57; DB 2; Length 1220;
Best Local Similarity 26.1%; Pred. No. 4,1e+02;
Matches 6; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNQXQXQLDDCCSXCNXXNX 26
DB 481 AGDHCEIDIDECASNPCLNGGHC 503

RESULT 65
T42218
Slit-1 protein homolog - rat
A;Alternate names: MEGF4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42218
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs in the rat slit-1 protein.
A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T42218
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1531 <NAK>
A;Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G3449289
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF4
C;Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein repeat

Query Match 47.5%; Score 57; DB 2; Length 1531;
Best Local Similarity 30.4%; Pred. No. 4.8e+02;
Matches 7; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNQXQXQLDDCCSXCNXXNX 26
DB 957 KGRNCEVSLDSCSSNPGCGGTC 979

RESULT 66
S23244
Hypothetical protein ZK643.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

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F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-33/Domain: propeptide #status predicted <PRO>
F;34-1810/Product: tenascin 230K #status predicted <MAT>
F;223-249/Domain: EGF homology <EGF1>
F;316-342/Domain: EGF homology <EGF>
F;592-673/Domain: fibronectin type III repeat homology <FN3A>
F;681-765/Domain: fibronectin type III repeat homology <FN3B>
F;773-857/Domain: fibronectin type III repeat homology <FN3C>
F;865-949/Domain: fibronectin type III repeat homology <FN3D>
F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
F;1046-1128/Domain: fibronectin type III repeat homology <FN3F>
F;1137-1219/Domain: fibronectin type III repeat homology <FN3G>
F;1228-1310/Domain: fibronectin type III repeat homology <FN3H>
F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
F;1407-1487/Domain: fibronectin type III repeat homology <FN3J>
F;1495-1575/Domain: fibronectin type III repeat homology <FN3K>
F;1590-1798/Domain: fibronogen beta/gamma homology <FBG>
F;1734-1747/Domain: calcium binding #status predicted <CAB>

Query Match 47.1%; Score 56.5; DB 1; Length 1810;
Best Local Similarity 29.7%; Pred. No. 5.9e+02;
Matches 11; Conservative 9; Mismatches 4; Indels 13; Gaps 2;

QY 4 XNQCXQXQL-----DDC-----CSXXCNXXNXC 27
      : : : : : ||| | : : : : :
DB 353 GNGRCENGLCVCHGFGVGDPCSKRCPKTCNNRGCV 389

RESULT 68
S38335
metallothionein - stone loach
C;Species: Noemacheilus barbatulus (stone loach)
C;Date: 18-Feb-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S38335; S17176; S15505
R;Kille, P.; Kay, J.; Sweeney, G.E.
Biochim. Biophys. Acta 1216, 55-64, 1993
A;Title: Analysis of regulatory elements flanking metallothionein genes in Cd-tolerant fish
A;Reference number: S38334; MUID:94032489; PMID:8218416
A;Accession: S38335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <K1>
A;Cross-references: UNIPROT:P25128; EMBL:X70043
R;Kille, P.; Stephens, P.E.; Kay, J.
Biochim. Biophys. Acta 1089, 407-410, 1991
A;Title: Elucidation of cDNA sequences for metallothioneins from rainbow trout, stone loach
A;Reference number: S16996; MUID:91316146; PMID:1859844
A;Accession: S17176
A;Molecule type: mRNA
A;Residues: 1-4,'E',6-60 <K12>
A;Cross-references: EMBL:X59393
C;Genetics:
A;Introns: 9/1; 31/1
C;Superfamily: metallothionein
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 46.7%; Score 56; DB 2; Length 60;
Best Local Similarity 26.9%; Pred. No. 67;
Matches 7; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQXLDCCSXCNXXNXC 26
      : : : : : ||| : : : : :
DB 18 CKTCNQCTTCKXSCCSPGCGSKC 43

RESULT 69
S25775
testis-specific protein Mst84d - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S25775; D56565
R;Kuhn, R.; Kuhn, C.; Boersch, D.; Glaetzer, K.H.; Schaefer, U.; Schaefer, M.
Mech. Dev. 35, 143-151, 1991

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homeotic protein dlk - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S53718
 R:Lee, Y.L.; Helman, L.; Hoffman, T.; Laborda, J.
 Biochim. Biophys. Acta 1261, 223-232, 1995
 A:Title: dlk, PG2 and Pref-1 mRNAs encode similar proteins belonging to the EGF-like superfamily
 A:Reference number: S53716; MUID:95226449; PMID:7711066
 A:Accession: S53718
 A:Molecule type: mRNA
 A:Residues: 1-385 <LEE>
 A:Cross-references: UNIPROT:Q09163; EMBL:U15980; NID:g562107; PIDN:AA560495.1; PID:g562107
 C:Superfamily: preadipocyte factor 1; EGF homology
 C:Keywords: transmembrane protein
 F:54-85/Domain: EGF homology <EGF1>
 F:92-124/Domain: EGF homology <EGF>
 F:131-167/Domain: EGF homology <EGF3>
 F:214-246/Domain: EGF homology <EGX1>
 F:303-332/Domain: transmembrane #status predicted <TM1>

Query Match 46.7%; Score 56; DB 2; Length:385;
 Best Local Similarity 19.2%; Pred.No. 2.3e+02;
 Matches 5; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNXC 27
 Db 201 GFVDKTCRPSVNCASGQCQNGTCL 226

RESULT 75
 A54785
 preadipocyte factor 1 precursor, long form - mouse
 N:Alternate names: delta-like dlk homeotic protein; pref-1
 C:Species: Mus musculus (house mouse)
 C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
 C:Accession: A54785; A45484; A40746; S21585
 R:Smas, C.M.; Green, D.; Sul, H.S.
 Biochemistry 33, 9257-9265, 1994
 A:Title: Structural characterization and alternate splicing of the gene encoding the preadipocyte factor 1 precursor
 A:Reference number: A54785; MUID:94325292; PMID:7519443
 A:Accession: A54785
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-385 <SMA>
 A:Cross-references: UNIPROT:Q09163; GB:S71340
 R:Laborda, J.; Sauvillie, E.A.; Hoffman, T.; Notario, V.
 J. Biol. Chem. 268, 3817-3820, 1993
 A:Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell carcinoma
 A:Reference number: A45484; MUID:93179372; PMID:8095043
 A:Accession: A45484
 A:Molecule type: mRNA
 A:Residues: 1-78, 'G', '80-343, 'TF', '346-385 <LAB>
 A:Cross-references: EMBL:212171; NID:g50716; PIDN:CAA78162.1; PID:g50717
 A:Note: sequence extracted from NCBI backbone (NCBIP:125734)
 A:Note: species designations for this sequence report and for B45484 originally were transferred from NCBI backbone
 R:Smas, C.M.; Sul, H.S.
 Cell 73, 725-734, 1993
 A:Title: Pref-1, a protein containing EGF-like repeats, inhibits adipocyte differentiation
 A:Reference number: A40746; MUID:93272313; PMID:8500166
 A:Accession: A40746
 A:Molecule type: mRNA
 A:Residues: 1-78, 'G', '80-249, 'P', '251-319, 'CWAPWPFSSFTSAKPGCPCTATTCTCFARRRTSCCSITAARSWRSISS
 A:Cross-references: GB:I12721; NID:g309092; PIDN:AAA37175.1; PID:g309093
 A:Experimental source: 3T3-L1 preadipocytes
 A:Note: this sequence appears to have been corrected in reference A45484
 C:Superfamily: preadipocyte factor 1; EGF homology
 F:1-385/Product: preadipocyte factor 1 precursor splice form A #status predicted <FOA>
 F:1-230, 282-385/Product: preadipocyte factor 1 precursor splice form B #status predicted
 F:1-230, 304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted
 F:1-230, 306-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted
 F:1-230, 304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted

F:1-210, 306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predicted
 F:92-124/Domain: EGF homology <EGF>
 F:214-246/Domain: EGF homology <EGF1>

Query Match 46.7%; Score 56; DB 2; Length 385;
 Best Local Similarity 19.2%; Pred.No. 2.3e+02;
 Matches 5; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDDCCSXCNXXNXC 27
 Db 201 GFVDKTCRPSVNCASGQCQNGTCL 226

RESULT 76
 T21421
 hypothetical protein F26E4.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21421
 R:Lightning, J.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19419
 A:Accession: T21421
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-491 <WIL>
 A:Cross-references: UNIPROT:P90850; EMBL:Z81070; PIDN:CAB03007.1; GSPDB:GN00019; CESP:F26E4
 A:Experimental source: clone F26E4
 C:Genetics:
 A:Gene: CESP:F26E4.3
 A:Map position: 1
 A:Introns: 23/3; 67/1; 108/1; 134/1; 149/2; 179/2; 232/2; 261/2; 306/2; 334/2; 419/2; 461/2

Query Match 46.7%; Score 56; DB 2; Length 491;
 Best Local Similarity 23.1%; Pred.No. 2.8e+02;
 Matches 6; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 CXIXNQXQXQLDDCCSXCNXXNXC 26
 Db 70 CSVRTHTCENRDDCTVPILGDHLC 95

RESULT 77
 S23408
 prematurely terminated mRNA decay factor NAM7 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YN9583.05c; protein YMR080c; UPF1 protein
 C:Species: Saccharomyces cerevisiae
 C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
 C:Accession: S23408; A44388; S54455
 R:Altamura, N.; Groudinsky, O.; Dujardin, G.; Slonimski, P.P.
 J. Mol. Biol. 224, 575-587, 1992
 A:Title: NAM7 nuclear gene encodes a novel member of a family of helicases with a Zn-ligand
 A:Reference number: S23408; MUID:92235815; PMID:1314899
 A:Accession: S23408
 A:Molecule type: DNA
 A:Residues: 1-971 <ALT>
 A:Cross-references: UNIPROT:P30771; EMBL:X62394; NID:g4022; PIDN:CAA44266.1; PID:g4023
 R:Leeds, P.; Wood, J.M.; Lee, B.S.; Culbertson, M.R.
 Mol. Cell. Biol. 12, 2165-2177, 1992
 A:Title: Gene products that promote mRNA turnover in Saccharomyces cerevisiae.
 A:Reference number: A44388; MUID:92236591; PMID:1569946
 A:Accession: A44388
 A:Molecule type: DNA
 A:Residues: 1-971 <LEE>
 A:Cross-references: GB:M76659; NID:gl73141; PIDN:AAA35197.1; PID:gl73142
 R:Gentles, S.; Bowman, S.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54451
 A:Accession: S54455
 A:Molecule type: DNA
 A:Residues: 1-971 <GEN>
 A:Cross-references: EMBL:Z49259; NID:g807956; PID:g807962; MIPS:YMR080C
 A:Experimental source: strain AB972

A:Molecule type: mRNA
A:Residues: 1-228,302-383 <LEE2>
A:Cross-references: EMBL:UI5981; NID:g562109; PIDN:AAA75365.1; PID:g562110
R:Laborada, J.
submitted to the EMBL Data Library, October 1994
A:Reference number: S71068
A:Accession: S71068

A:Molecule type: mRNA
A:Residues: 1-344,346-383 <LAB1>
A:Cross-references: EMBL:UI5979; NID:g562105; PIDN:AAA75364.1; PID:g562106
R:Laborada, J.; Sauville, E.A.; Hoffman, T.; Notario, V.
J. Biol. Chem. 268, 3817-3820, 1993
A>Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell
A:Reference number: A45484; MUID:93179372; PMID:8095043
A:Accession: B45484

A:Molecule type: mRNA
A:Residues: 1-45,'HV',48-383 <LAB2>
A:Cross-references: EMBL:I212172; NID:g38478; PIDN:CAA78163.1; PID:g38479
A>Note: sequence extracted from NCBI backbone (NCBIP:125735)
R>Jensen, C.H.; Krogh, T.N.; Hojrup, P.; Clausen, P.P.; Skjodt, K.; Larsson, L.I.; Englund,
E.J. Biochem. 225, 83-92, 1994
A>Title: Protein structure of fetal antigen 1 (FAL). A novel circulating human epidermal
pg2.
A:Reference number: S487113; MUID:95010145; PMID:7925474
A:Accession: S487113

A:Molecule type: protein
A:Residues: 24-107,'D',109-282 <JEN>
R:Hojrup, P.; Jensen, C.H.; Skjodt, K.; Teisner, B.
Protein Sci. 2(Suppl.1), 259S, 1993
A>Title: Primary structure of human fetal antigen 1 (FAL), a putative homeotic glycoprotein
A:Reference number: A44549
A:Accession: A44549
A>Status: preliminary

A:Molecule type: protein
A:Residues: 24-107,'VASM',112-283 <HOJ>
C:Genetics:
A:Gene: GDB:DLL1; dlk; FAL; PG2; PREF-1
A:Cross-references: GDB:9958854; OMIM:176290
A:Map position: 14q32-14q32
C:Superfamily: preadipocyte factor 1; EGF homology
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:21-54/Domain: EGF homology #status atypical <EGF1>
F:24-38/Product: delta-like homeotic protein dlk, long splice form #status predicted <MW>
F:24-283/Product: fetal antigen 1 #status experimental <WATA>
F:24-228,302-383/Product: delta-like homeotic protein dlk, short splice form #status predicted <MW>
F:57-85/Domain: EGF homology <EGF2>
F:92-124/Domain: EGF homology <EGF3>
F:131-167/Domain: EGF homology <EGF4>
F:174-205/Domain: EGF homology <EGF5>
F:212-244/Domain: EGF homology <EGF6>
F:305-327/Domain: transmembrane #status predicted <TRM>
F:94,214/Binding site: carbohydate (Ser) (covalent) #status experimental
F:100/Binding site: carbohydate (Asn) (covalent) #status experimental
F:134/Binding site: carbohydate (Asn) (covalent) #status absent
F:143/Binding site: carbohydate (Thr) (covalent) #status experimental
F:183,251,260/Binding site: carbohydate (Ser) (covalent) #status experimental
F:165,172/Binding site: carbohydate (Asn) (covalent) (partial) #status atypical
F:222/Binding site: carbohydate (Thr) (covalent)

Query Match 45.8%; Score 55; DB 2; Length 383;
Best Local Similarity 19.2%; Pred. No. 2.9e+02;
Matches 5; Conservative 16; Mismatches 5; Indels 0; Gaps 0;

OY 2 XIXNOXCXQLDDCCSXCNKXXNCVC 27
 : ::::|::::| |:::: ::
Db 199 GFIDKTCSRPTVNTCASSPCQNGGTCL 224

RESULT 89
T09456
intrinsic factor-B12 receptor Cubilin precursor - human
Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C/Accession: T09456
R/Kozyraki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998

A>Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A/Reference number: Z16677; UID:98241400; PMID:9572993

A/Accession: T09456

A>Status: preliminary; translated from GB/EMBL/DDJB

A/Molecule type: mRNA

A/Residues: 1-3623 <KOZ>

A/Cross-references: UNIPROT.O60494; EMBL.AFO34611; NID:g3929528; PIDN:AACB2612.1; PID:g3929528

C/Genetics:

C/Superfamily: 10pl12

C/A:Map position: intrinsc factor-B12 receptor cubilin; EGF homology

E/F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domian: EGF homology <EGF>

Query Match 45.8%; Score 55; DB 2; Length 3623;
Best Local Similarity 28.6%; Pred.No. 1.3e+03;
Matches 6; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Oy 7 XCQXQLDDCCSXCNXXNCV 27
| : | : | : | : ||
Db 428 NCTENINECLSNPLNGTGV 448

RESULT 90

NTHIRP
robustoxin - funnel-web spider (Atrax robustus)

C/Species: Atrox robustus
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004

C/Accession: A01738
R/Shumack, D.D.; Claassens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1985

A>Title: Complete amino acid sequence of a new type of lethal neurotoxin from the venom
A/Reference number: A01738; UID:85127480; PMID:3972101

A/Accession: A01738

A/Molecule type: protein

A/Residues: 1-42 <SHE>

A/Cross-references: UNIPROT.P01478

C/Comment: In this species, the venom of the male is lethal rather than that of the female.

C/Comment: Four disulfide bonds are present.

C/Superfamily: robustoxin

C/Keywords: neurotoxin; venom

Query Match 45.4%; Score 54.5; DB 1; Length 42;
Best Local Similarity 25.8%; Pred.No. 73;
Matches 8; Conservative 11; Mismatches 7; Indels 5; Gaps 1;

Oy 1 CXIXNQXCXQLDCCSXHC-----NXNNYC 26
| : | : | : | : ||
Db 1 CAKKRNWCGKNEGCCPKMKIYAWYNQQGSC 31

RESULT 91

NTHIV
versutoxin - funnel-web spider (Atrax versutus)

C/Species: Atrax versutus
C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004

C/Accession: S00343
R/Brown, M.R.; Shumack, D.D.; Tyler, M.I.; Howden, M.E.H.
Biochem. J. 250, 401-405, 1988

A>Title: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the funnel web spider (Atrax versutus).

A/Reference number: S00343; UID:88183359; PMID:3355530

A/Accession: S00343

A/Molecule type: protein

A/Residues: 1-42 <ERO>

A/Cross-references: UNIPROT.P13494

C/Comment: All cysteine residues are linked by disulfide bonds.

C/Superfamily: robustoxin

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09456
R/Kozyraki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A>Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A/Reference number: Z16677; UID:98241400; PMID:9572993
A/Accession: T09456
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-3623 <KOZ>
A/Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AACB2612.1; PID:g3929528
C/Genetics:
A/Map position: 10p12
C/Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C/Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 45.8%; Score 55; DB 2; Length 3623;
Best Local Similarity 28.6%; Pred.No. 1.3e+03;
Matches 6; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 7 KCXQLDDCCSXNCNNXXCV 27
 :|::|| |:: ||
Db 428 NCTENINECLSNPLNGTGV 448

RESULT 90
NTIIRF
robustoxin - funnel-web spider (Atrax robustus)
C/Species: Atrax robustus
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C/Accession: A01738
R/Shenumack, D.D.; Claassens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1985
A>Title: Complete amino acid sequence of a new type of lethal neurotoxin from the venom
A/Reference number: A01738; UID:85127480; PMID:3972101
A/Accession: A01738
A/Molecule type: protein
A/Residues: 1-42 <SHE>
A/Cross-references: UNIPROT:P01478
C/Comment: In this species, the venom of the male is lethal rather than that of the female.
C/Comment: Four disulfide bonds are present.
C/Superfamily: robustoxin
C/Keywords: neurotoxin; venom

Query Match 45.4%; Score 54.5; DB 1; Length 42;
Best Local Similarity 25.8%; Pred.No. 73;
Matches 8; Conservative 11; Mismatches 7; Indels 5; Gaps 1;

Qy 1 CXIXNQXCXQLDCCSXKC-----NXNYXC 26
 |:|::|| |:: ||
Db 1 CAKKRNWCKNECCCPCMKCIYAWYNQGSC 31

RESULT 91
NTIIIV
versutoxin - funnel-web spider (Atrax versutus)
C/Species: Atrax versutus
C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C/Accession: S00343
R/Brown, M.R.; Sheumack, D.D.; Tyler, M.I.; Howden, M.E.H.
Biochem. J. 250, 401-405, 1988
A>Title: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the funnel-web spider.
A/Reference number: S00343; UID:88183358; PMID:3355530
A/Accession: S00343
A/Molecule type: protein
A/Residues: 1-42 <BRO>
A/Cross-references: UNIPROT:P13494
C/Comment: All cysteine residues are linked by disulfide bonds.
C/Superfamily: robustoxin

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T09456
R/Kozyraki, R.; Kristiansen, M.; Silahatoglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N.
Blood 91, 3593-3600, 1998
A>Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characterization.

A/Reference number: Z16677; UID:98241400; PMID:9572993
A/Accession: T09456
A>Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-3623 <KOZ>
A/Cross-references: UNIPROT:O60494; EMBL:AF034611; NID:g3929528; PIDN:AACB2612.1; PID:g3929528
C/Genetics:

C/Superfamily: 10pl12
A:Map position: intrinsc factor-B12 receptor cubilin; EGF homology
C/Keywords: receptor; vitamin B12 uptake
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F:436-467/Domain: EGF homology <EGF>

Query Match 45.8% Score 55; DB 2; Length 3623;
Best Local Similarity 28.6%; Pred.No. 1.3e+03;
Matches 6; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 7 KCXQLDDCCSXNCNNXXCV 27
 :|::||| |::| ::||
Db 428 NCTENINECLSNPLNGTGV 448

RESULT 90
NTIIRF
robustoxin - funnel-web spider (Atrax robustus)
C/Species: Atrax robustus
C/Date: 27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change 09-Jul-2004
C/Accession: A01738
R/Shuumack, D.D.; Claassens, R.; Whiteley, N.M.; Howden, M.E.H.
FEBS Lett. 181, 154-156, 1985
A>Title: Complete amino acid sequence of a new type of lethal neurotoxin from the venom
A/Reference number: A01738; UID:85127480; PMID:3972101
A/Accession: A01738
A:Molecule type: protein
A/Residues: 1-42 <SHE>
A/Cross-references: UNIPROT:P01478
C/Comment: In this species, the venom of the male is lethal rather than that of the female.
C/Comment: Four disulfide bonds are present.
C/Superfamily: robustoxin
C/Keywords: neurotoxin; venom

Query Match 45.4% Score 54.5; DB 1; Length 42;
Best Local Similarity 25.8%; Pred.No. 73;
Matches 8; Conservative 11; Mismatches 7; Indels 5; Gaps 1;

Qy 1 CXIXNQXCXLDDCCSXKC-----NXNYXC 26
 |:|::||| ||::| |::|
Db 1 CAKKRNWCKNEDECCCPMKCIYAWYNQQGSC 31

RESULT 91
NTIIIV
versutoxin - funnel-web spider (Atrax versutus)
C/Species: Atrax versutus
C/Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C/Accession: S00343
R/Brown, M.R.; Shuumack, D.D.; Tyler, M.I.; Howden, M.E.H.
Biochem. J. 250, 401-405, 1988
A>Title: Amino acid sequence of versutoxin, a lethal neurotoxin from the venom of the funnel-web spider.
A/Reference number: S00343; UID:88183358; PMID:3355530
A/Accession: S00343
A:Molecule type: protein
A/Residues: 1-42 <BRO>
A/Cross-references: UNIPROT:P13494
C/Comment: All cysteine residues are linked by disulfide bonds.
C/Superfamily: robustoxin

Cross-references: UNIPROT:P15799; GB:M83937; NID:q159124

Product	Form	#status	predicted
1-1779, 1788-1959/	agrin,	form 3	<AG3>
1-1779, 1788-1959/	agrin,	form 5	<AG5>

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Qy 1 CXIXNQXC---XQXLDCCSXCNXNXC 27
      | : : : | : : : | : : : | : : : | :
Db 1065 CTKSQVCQDKMQLDGLDDEHCNEEKCL 1094

RESULT 99
I51538
metallothionein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51538
R:Saint-Jacques, E.; Seguin, C.
DNA Cell Biol 12, 329-340, 1993
A:Title: Cloning and nucleotide sequence of a complementary DNA encoding Xel
A:Reference number: I51538; MUID:93263990; PMID:8494609
A:Accession: I51538
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-62 <SAIL>
A:Cross-references: UNIPROT:Q05890; GB:M96729; NID:g214585; PIDN:AA859949.1
C:Superfamily: metallothionein

Query Match 45.0%; Score 54; DB 2; Length 62;
Best Local Similarity 26.9%; Pred. No. 1.1e+02;
Matches 7; Conservative 11; Mismatches 8; Indels 0; Gaps

Qy 1 CXIXNQXCXQXLDCCSXCNXNXC 26
      | : : | : : : | : : : | : : :
Db 20 CSCSNCKTCKKSCCPCPAECSKC 45

RESULT 100
T11547
metallothionein - purple sea urchin (fragment)
C:Species: Sphaerechinus granularis (purple sea urchin)
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T11547
R:Scudiero, R.; Parisi, E.
submitted to the EMBL Data Library, October 1995
A:Description: Isolation, characterization and deduction of primary structure
A:Reference number: Z17282
A:Accession: T11547
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-67 <SCU>
A:Cross-references: UNIPROT:Q26497; EMBL:Z66530; NID:gl045269; PID:gl045270
C:Superfamily: metallothionein
C:Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 45.0%; Score 54; DB 2; Length 67;
Best Local Similarity 26.9%; Pred. No. 1.1e+02;
Matches 7; Conservative 11; Mismatches 8; Indels 0; Gaps

```

```

DD      23  CC1GSCCAGGGGGLCCGKCSNNAACNC  48
Search completed: April 18, 2005, 20:38:44
Job time : 29.5 secs

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Match 45.4%; Score 54.5; DB 2; Length 2643;
Local Similarity 30.0%; Pred. NO. 1.2e+03;
9; Conservative 12; Mismatches 6; Indels 3; Caps 1;

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: April 18, 2005, 20:00:51 ; Search time 117 Seconds
(without alignments)
118.172 Million cell updates/sec

Title: US-10-627-685A-1
Perfect score: 120
Sequence: 1 CXIXNQXCXQLDDCCSXXCNXXNCV 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	120	100.0	67	2	Q71KT2 conus purpu
2	120	100.0	72	1	CXK7 CONPU
3	77	64.2	72	1	CXOB CONST
4	73	60.8	26	1	CXOC CONST
5	72	60.0	2524	1	NOTC_XENLA
6	69	57.5	29	1	CXOC_CONMA
7	69	57.5	1820	2	Q6LFW8
8	68	56.7	74	2	Q646U5
9	68	56.7	74	2	Q646U7
10	68	56.7	1961	2	Q6MG89
11	68	56.7	2556	1	NTC1_HUMAN
12	67	55.8	487	2	Q8MSX5
13	67	55.8	778	2	Q91BG4
14	67	55.8	2139	1	CRB_DROME
15	67	55.8	2146	2	Q9VC97
16	67	55.8	2437	1	NTC1_BRARE
17	67	55.8	2516	2	Q7TQ52
18	67	55.8	2526	2	Q7TQ51
19	67	55.8	2531	1	NTC1_MOUSE
20	67	55.8	2531	1	NTC1_RAT
21	67	55.8	2531	2	Q8K428
22	67	55.8	2531	2	Q7TQ50
23	66	55.0	664	2	Q91AT6
24	66	55.0	721	2	Q91S02
25	66	55.0	1317	2	Q61Q50
26	66	55.0	1551	2	Q9NGV4
27	66	55.0	2447	2	O13149
28	66	55.0	2470	1	NTC2_MOUSE
29	66	55.0	2471	1	NTC2_HUMAN
30	66	55.0	2471	1	NTC2_RAT
31	66	55.0	2528	2	Q8AXP0

32	66	55.0	2703	1	NOTC_DROME
33	66	55.0	3396	2	Q9VM55
34	65	54.2	726	2	Q8AW87
35	65	54.2	752	2	Q42374
36	65	54.2	1075	2	Q9NC90
37	65	54.2	1214	2	Q90YD2
38	65	54.2	1290	2	Q9M6E1
39	65	54.2	1410	2	Q20204
40	65	54.2	1964	1	NTC4_MOUSE
41	65	54.2	2318	1	NTC3_MOUSE
42	65	54.2	2319	1	NTC3_RAT
43	65	54.2	2321	1	NTC3_HUMAN
44	65	54.2	2531	2	O16004
45	65	54.2	2533	2	Q25253
46	64.5	53.8	74	2	Q646V4
47	64.5	53.8	74	2	Q646V5
48	64.5	53.8	74	2	Q646W1
49	64	53.3	647	2	Q6P3V5
50	64	53.3	838	2	Q9VQA9
51	64	53.3	1372	2	P91526
52	64	53.3	2003	1	NTC4_HUMAN
53	64	53.3	2352	2	O61240
54	64	53.3	3623	2	O70244
55	63	52.5	43	1	MTB_COLVI
56	63	52.5	570	1	FBP3_STRPU
57	63	52.5	585	2	Q8OW06
58	63	52.5	587	2	Q8NBS4
59	63	52.5	589	1	DLI3_RAT
60	63	52.5	592	1	DLI3_MOUSE
61	63	52.5	618	1	DLI3_HUMAN
62	63	52.5	642	2	P79941
63	63	52.5	642	2	P79941
64	63	52.5	1202	1	JAG2_RAT
65	63	52.5	1238	1	JAG2_HUMAN
66	63	52.5	1247	1	JAG2_MOUSE
67	63	52.5	1687	2	O61204
68	63	52.5	3523	2	Q7QCP4
69	62	51.7	29	1	CXO7_CONGE
70	62	51.7	62	2	Q71KS8
71	62	51.7	71	1	CXOD_CONCT
72	62	51.7	74	2	Q646U3
73	62	51.7	74	2	Q646U4
74	62	51.7	74	2	Q646W2
75	62	51.7	74	2	Q646W3
76	62	51.7	74	2	Q646W6
77	62	51.7	153	2	Q9AUD1
78	62	51.7	382	1	EFL9_MOUSE
79	62	51.7	383	1	EFL9_HUMAN
80	62	51.7	638	2	Q7PM27
81	62	51.7	713	2	Q962W9
82	62	51.7	714	1	DLI1_RAT
83	62	51.7	722	1	DLI1_MOUSE
84	62	51.7	722	2	Q6PFV7
85	62	51.7	723	1	DLI1_HUMAN
86	62	51.7	824	1	FBP1_STRPU
87	62	51.7	1064	1	FBP1_STRPU
88	62	51.7	1286	2	Q7QCT2
89	62	51.7	1515	2	Q9DE37
90	62	51.7	1685	2	Q9U4A2
91	62	51.7	2037	2	Q7QFS2
92	62	51.7	2428	2	Q816X6
93	62	51.7	2524	2	Q9GPA5
94	61.5	51.2	36	1	TXM1_AGEAP
95	61.5	51.2	81	2	Q9BP77
96	61.5	51.2	471	2	O8LAG1
97	61.5	51.2	471	2	O8VZE5
98	61.5	51.2	481	2	O9ZVZ7
99	61.5	51.2	2050	2	Q81K03
100	61	50.8	29	1	CXOD_CONMA

ALIGNMENTS

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RESULT 1
Q71KT2
ID Q71KT2 PRELIMINARY; PRT; 67 AA.
AC Q71KT2
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F., Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480312; AAQ05864.1; -
DR HSSP; P56633; IAV3.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41 67 four-loop conotoxin.
SQ SEQUENCE 67 AA; 7712 MW; E7E77CG61873E1DB CRC64;

Query Match 100.0%; Score 120; DB 2; Length 67;
Best Local Similarity 63.0%; Pred. No. 6e-05;
Matches 17; Conservative 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXIXNQXQXQLDDCCSXKCNXXNXCVCV 27
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 41 CRIPNQKCFQHLDDCCSRKCNRFNKCVCV 67

RESULT 2
CXK7 CONPU
ID -CXK7 CONPU STANDARD; PRT; 72 AA.
AC P56633;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.
RA Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
RA Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,
RA Olivera B.M.;
RT "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
channel.";
RL J. Biol. Chem. 273:33-38 (1998).
RN [2]
RP SEQUENCE OF 46-72, AND SYNTHESIS.
RX MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;
RA Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,
RA Olivera B.M.;
RT "Strategy for rapid immobilization of prey by a fish-hunting marine
snail.";
RL Nature 381:148-151 (1996).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9;
RA Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,

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RA Craik D.J.;
RT "Solution structure and proposed binding mechanism of a novel
RT potassium channel toxin kappa-conotoxin PVIIA.";
RL Structure 5:1585-1597 (1997).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341;
RA Savarin P., Guenneugues M., Gilquin B., Lamthanh H., Gasparini S.,
RA Zinn-Juatin S., Menez A.;
RT "Three-dimensional structure of kappa-conotoxin PVIIA, a novel
RT potassium channel-blocking toxin from cone snails.";
RL Biochemistry 37:5407-5416 (1998).
RN [5]
RP MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54;
RP PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63;
RP LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.
RX MEDLINE=20387358; PubMed=10818087; DOI=10.1074/jbc.C900990199;
RA Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J.,
RA Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.;
RT "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt
RT interaction with the shaker K+ channel.";
RL J. Biol. Chem. 275:24639-24644 (2000).
RN [6]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=99329121; PubMed=10398696;
RA Terlau H., Boccaccio A., Olivera B.M., Conti F.;
RT "The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
RT dependent.";
RL J. Gen. Physiol. 114:125-140 (1999).
RN [7]
RP MODEL OF THE SHAKER-PVIIA INTERACTION.
RX MEDLINE=21678121; PubMed=11820396;
RA Moran O.;
RT "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with
RT the shaker potassium channel pore.";
RL Eur. Biophys. J. 30:528-536 (2001).
RN [8]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=22017751; PubMed=12023223;
RA Naranjo D.;
RT "Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.";
RL Biophys. J. 82:3003-3011 (2002).
CC -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
CC potassium channels. The rat brain voltage-gated potassium channel
CC protein Kv1.1 is resistant to this toxin, but the voltage-gated
CC potassium channel protein Shaker (Drosophila) is sensitive. The
CC interaction site between the Shaker channel and this toxin is
CC within the S5-S6 loop of the Shaker channel. In fish, this toxin
CC induces hyperactivity, followed by continuous contraction and
CC extension of major fins, without immobilization or death.
CC Injection of this peptide together with the delta-conotoxin PVIA
CC causes the sudden tetanus of prey (STOP) syndrome, which is a
CC single, lethal "fin-pop" in envenomated fish. In mice, induces
CC hyperactivity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=3268.4; METHOD=PAB; RANGE=46-72; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
CC family.
CC -!- CAUTION: Because analogs resulting of mutagenesis of Hyp-49, Asn-
CC 50, Ieu-57 and Asp-59 gave very low yields upon folding, the
CC results of mutagenesis on these residues should be interpreted
CC with caution.
DR PIR; A58997; A58997.
DR PDB; 1AV3; NMR; @=1-27.
DR PDB; 1KCP; NMR; @=1-27.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR 3D-structure; Direct protein sequencing; Hydroxylation;
KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
FT SIGNAL; Toxin.
FT PROPEP 1 22 Potential.
FT 23 45

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RL J. Biol. Chem. 275:35335-35344 (2000).
 CC -|- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC) (By
 CC similarity). This toxin blocks N-, P-, and Q-type calcium
 CC channels.
 CC -|- SUBCELLULAR LOCATION: Secreted.
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -|- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
 CC family.
 DR HSSP; P05484; 1DW4.
 KW Amidation; Calcium channel inhibitor; Direct protein sequencing;
 FW Ionic channel inhibitor; Neurotoxin; presynaptic neurotoxin; Toxin.
 FT DISULFID 1 16 By similarity.
 FT DISULFID 8 20 By similarity.
 FT DISULFID 15 26 By similarity.
 FT MOD_RES 26 26 Cysteine amide.
 SQ SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;
 Query Match 60.8%; Score 73; DB 1; Length 26;
 Best Local Similarity 30.8%; Pred. No. 1-3;
 Matches 8; Conservative 14; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 CXIXNXXCXQLDCCSXCNXXNC 26
 Db 1 CKRGQSCSKLMDCTGCSRRGKC 26
 RESULT 5
 NOTC_XENLA STANDARD; PRT; 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurogenic locus notch protein homolog precursor (XOTCH protein).
 GN Name=XOTCH;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385285; PubMed=2402639;
 RA Coffman C., Harris W., Kintner C.;
 RT "Xotch, the Xenopus homolog of Drosophila notch."; Science 249:1438-1441 (1990).
 RL [2]
 RP REVISIONS TO 1759-1782.
 RA Kintner C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- DEVELOPMENTAL STAGE: Expressed almost uniformly in early embryos.
 CC -|- SIMILARITY: Belongs to the NOTCH family.
 CC -|- SIMILARITY: Contains 6 ANK repeats.
 CC -|- SIMILARITY: Contains 36 EGF-like domains.
 CC -|- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M33874; AAB02039.1; -.
 DR HSSP; P46531; 1PB5.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; ASX_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 36.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGF_BLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; Ank; 6.
 DR SMART; SM00179; EGF_Ca; 24.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS0297; ANK_REPEAT; 4.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 23.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 29.
 DR PROSITE; PS00026; EGF_3; 36.
 DR PROSITE; PS01187; EGF_Ca; 21.
 KW ANK repeat; Differentiation; EGF-like domain; Glycoprotein;
 KW Neurogenesis; Notch signaling pathway; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 2524 Neurogenic locus notch protein homolog.
 FT DOMAIN 20 1728 Extracellular (Potential).
 FT TRANSMEM 1729 1750 Potential.
 FT DOMAIN 1751 2524 Cytoplasmic (Potential).
 FT DOMAIN 20 57 EGF-like 1.
 FT DOMAIN 58 99 EGF-like 2.
 FT DOMAIN 102 140 EGF-like 3.
 FT DOMAIN 141 177 EGF-like 4.
 FT DOMAIN 179 215 EGF-like 5.
 FT DOMAIN 217 254 EGF-like 6.
 FT DOMAIN 256 292 EGF-like 7.
 FT DOMAIN 294 332 EGF-like 8.
 FT DOMAIN 334 370 EGF-like 9.
 FT DOMAIN 371 409 EGF-like 10.
 FT DOMAIN 411 449 EGF-like 11.
 FT DOMAIN 451 487 EGF-like 12.
 FT DOMAIN 489 525 EGF-like 13.
 FT DOMAIN 527 563 EGF-like 14.
 FT DOMAIN 565 600 EGF-like 15.
 FT DOMAIN 602 638 EGF-like 16.
 FT DOMAIN 640 675 EGF-like 17.
 FT DOMAIN 677 713 EGF-like 18.
 FT DOMAIN 715 750 EGF-like 19.
 FT DOMAIN 752 788 EGF-like 20.
 FT DOMAIN 790 826 EGF-like 21.
 FT DOMAIN 828 866 EGF-like 22.
 FT DOMAIN 868 904 EGF-like 23.
 FT DOMAIN 906 942 EGF-like 24.
 FT DOMAIN 944 980 EGF-like 25.
 FT DOMAIN 982 1018 EGF-like 26.
 FT DOMAIN 1020 1056 EGF-like 27.
 FT DOMAIN 1058 1094 EGF-like 28.
 FT DOMAIN 1096 1142 EGF-like 29.
 FT DOMAIN 1144 1180 EGF-like 30.
 FT DOMAIN 1182 1218 EGF-like 31.
 FT DOMAIN 1220 1264 EGF-like 32.
 FT DOMAIN 1266 1304 EGF-like 33.
 FT DOMAIN 1306 1346 EGF-like 34.
 FT DOMAIN 1347 1383 EGF-like 35.
 FT DOMAIN 1386 1424 EGF-like 36.
 FT REPEAT 1441 1478 Lin/Notch 1.
 FT REPEAT 1479 1520 Lin/Notch 2.
 FT REPEAT 1521 1560 Lin/Notch 3.
 FT REPEAT 1562 1599 ANK 1.
 FT REPEAT 1600 1637 ANK 2.
 FT REPEAT 1638 1675 ANK 3.
 FT REPEAT 1676 1713 ANK 4.
 FT REPEAT 1714 1751 ANK 5.

100

W

du Z., BOS J.I.B., Armstrong M., Whisson S.C., da Cunha L.,

DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 10.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 21.
DR PROSITE; PS00026; EGF_3; 27.
DR PROSITE; PS01187; EGF_CA; 9.
DR PROSITE; PS00200; RIESKE_2; UNKNOWN_1.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 1961 AA; 206074 MW; 5B1034E9BE07A3C CRC64;

Query Match 56.7%; Score 68; DB 2; Length 1961;
Best Local Similarity 29.2%; Pred. No. 2e+02;
Matches 7; Conservative 14; Mismatches 3; Indels 0; Gaps

QY 4 XNQXCXQLDDCCSXCNXXNXCVCV 27
: :|::||| ::| ::|:
Db 345 GGEGCDENLDCAAAATCALGSTCI 368

RESULT 11
NTCL HUMAN NTCL HUMAN STANDARD; PRT; 2556 AA.

ID NTCL HUMAN ID NTCL HUMAN STANDARD; PRT; 2556 AA.
AC P46531;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
DE (Translocation-associated notch protein TAN-1).
GN Name=NOTCH1; Synonyms=TAN1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mann R.S., Blumweller C.M., Zagouras P.;
RT "Complete human notch 1 (hnl) cDNA sequence."
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
[2]
RP SEQUENCE OF 1-2444 FROM N.A.
RX MEDLINE=91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B;
RX Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,
RX Smith S.D., Sklar J.;
RA "TAN-1, the human homolog of the Drosophila notch gene, is broken by
RT chromosomal translocations in T lymphoblastic neoplasms.";
RT Cell 66:649-661(1991).
RN [3]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=98250176; PubMed=10079256;
RX Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangi M.-L.,
RX Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RA "Human ligands of the Notch receptor."
RT Ann. J. Pathol. 154:785-794(1999).
RN [4]
RP INTERACTION WITH DTG1.
RX MEDLINE=98250176; PubMed=9590294;
RX Matsuno K., Eastman D., Mitsiades T., Quinn A.M., Carcangi M.L.,
RX Ordentlich P., Kadesch T., Artavanis-Tsakonas S.;
RA "Human deltex is a conserved regulator of Notch signalling."
RT Nat. Genet. 19:74-78(1998).

-!- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May be important for normal lymphocyte function. In altered form, may contribute to transformation or progression in some T-cell neoplasms. Involved in the maturation of both CD4+ and CD8+ cells in the thymus (By similarity).
-!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(IEC) which are probably linked by disulfide

CC bonds (By similarity). Interacts with DTX1 and DTX2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus (By
 CC similarity).
 CC -!- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
 CC brain stem and lung. Also present in most adult tissues where it
 CC is found mainly in lymphoid tissues.
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(1M) and a N-terminal fragment N(1C). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (N(1XT)). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- DISEASE: NOTCH1 truncation is associated with T-cell acute
 CC lymphoblastic leukemia.
 CC -!- SIMILARITY: Belongs to the NOTCH family.
 CC -!- SIMILARITY: Contains 5 ANK repeats.
 CC -!- SIMILARITY: Contains 36 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 CC EMBL; AF308602; AAC33848.1; .
 CC EMBL; M73980; AAA60614.1; .
 CC PDB; 1PB5; NMR; A=1447-1481.
 CC Genew; HGNC:7881; NOTCH1.
 CC MIM; 190198; .
 CC GO; GO:0016021; C: integral to membrane; NAS.
 CC GO; GO:0006955; P: immune response; NAS.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR00152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001438; EGF_II.
 CC InterPro; IPR006209; EGF_Like.
 CC InterPro; IPR010660; NOD.
 CC InterPro; IPR008297; Notch.
 CC InterPro; IPR008080; Notch_region.
 CC Pfam; PF00023; Ank; 6.
 CC Pfam; PF00008; EGF; 35.
 CC Pfam; PF06816; NOD; 1.
 CC Pfam; PF00066; Notch; 3.
 CC PIRSF; PIRSF02279; Notch; 1.
 CC PRINTS; PR01415; ANKYRIN.
 CC PRINTS; PR00010; EGFBLD.
 CC PRINTS; PR01452; NOTCH.
 CC SMART; SM00248; ANK; 6.
 CC SMART; SM00179; EGF_CA; 23.
 CC SMART; SM00004; NL; 3.
 CC PROSITE; PS00088; ANK_REPEAT; 4.
 CC PROSITE; PS00297; ANK_REPEAT_REGION; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 20.
 CC PROSITE; PS00022; EGF_1; 34.
 CC PROSITE; PS01186; EGF_2; 26.
 CC PROSITE; PS00026; EGF_3; 36.
 CC PROSITE; PS01187; EGF_CA; 18.
 CC 3D-structure; Activator; ANK repeat; Developmental protein;
 CC Differentiation; EGF-like domain; Glycoprotein;
 CC Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal;
 CC Transcription regulation; Transmembrane.
 CC SIGNAL 1 18 Potential.

FT CHAIN	19	2556	Neurogenic locus notch homolog protein 1.
FT CHAIN	1722	2556	Notch extracellular truncation (By
FT			similarity).
FT CHAIN	1755	2556	Notch intracellular domain (By
FT			similarity).
FT DOMAIN	19	1736	Extracellular (Potential).
FT TRANSMEM	1737	1757	Potential.
FT DOMAIN	1758	2556	Cytoplasmic (Potential).
FT DOMAIN	20	58	EGF-like 1.
FT DOMAIN	59	99	EGF-like 2.
FT DOMAIN	102	139	EGF-like 3.
FT DOMAIN	140	176	EGF-like 4.
FT DOMAIN	178	216	EGF-like 5.
FT DOMAIN	218	255	EGF-like 6.
FT DOMAIN	257	293	EGF-like 7.
FT DOMAIN	295	333	EGF-like 8.
FT DOMAIN	335	371	EGF-like 9.
FT DOMAIN	372	410	EGF-like 10.
FT DOMAIN	412	450	EGF-like 11.
FT DOMAIN	450	488	EGF-like 12.
FT DOMAIN	490	526	EGF-like 13.
FT DOMAIN	528	564	EGF-like 14.
FT DOMAIN	565	601	EGF-like 15.
FT DOMAIN	603	639	EGF-like 16.
FT DOMAIN	641	676	EGF-like 17.
FT DOMAIN	678	714	EGF-like 18.
FT DOMAIN	716	751	EGF-like 19.
FT DOMAIN	753	789	EGF-like 20.
FT DOMAIN	791	827	EGF-like 21.
FT DOMAIN	829	868	EGF-like 22.
FT DOMAIN	870	906	EGF-like 23.
FT DOMAIN	908	944	EGF-like 24.
FT DOMAIN	946	982	EGF-like 25.
FT DOMAIN	984	1020	EGF-like 26.
FT DOMAIN	1022	1058	EGF-like 27.
FT DOMAIN	1060	1096	EGF-like 28.
FT DOMAIN	1098	1144	EGF-like 29.
FT DOMAIN	1146	1182	EGF-like 30.
FT DOMAIN	1184	1220	EGF-like 31.
FT DOMAIN	1222	1266	EGF-like 32.
FT DOMAIN	1268	1306	EGF-like 33.
FT DOMAIN	1308	1347	EGF-like 34.
FT DOMAIN	1349	1385	EGF-like 35.
FT DOMAIN	1388	1427	EGF-like 36.
FT REPEAT	1446	1481	Lin/Notch 1.
FT REPEAT	1482	1523	Lin/Notch 2.
FT REPEAT	1524	1563	Lin/Notch 3.
FT REPEAT	1528	1597	ANK 1.
FT REPEAT	1561	1591	ANK 2.
FT REPEAT	1595	2024	ANK 3.
FT REPEAT	2028	2057	ANK 4.
FT REPEAT	2061	2090	ANK 5.
FT DOMAIN	1576	1579	Poly-Val.
FT DOMAIN	1562	1665	Poly-Arg.
FT DOMAIN	1729	1732	Poly-Pro.
FT DOMAIN	1741	1744	Poly-Ala.
FT DOMAIN	1902	1905	Poly-Glu.
FT DOMAIN	2260	2263	Poly-Gly.
FT DOMAIN	2404	2407	Poly-Gln.
FT DOMAIN	2411	2418	Poly-Pro.
FT DOMAIN	2522	2525	Poly-Ser.
FT SITE	1665	1666	Cleavage (by furin-like protease) (By
FT			similarity).
FT DISULFID	24	37	By similarity.
FT DISULFID	31	46	By similarity.
FT DISULFID	48	57	By similarity.
FT DISULFID	63	74	By similarity.
FT DISULFID	68	87	By similarity.
FT DISULFID	89	98	By similarity.
FT DISULFID	106	117	By similarity.
FT DISULFID	111	127	By similarity.
FT DISULFID	129	138	By similarity.
FT DISULFID	144	155	By similarity.

RESULT 14
CRB_DROME
ID CRB D

FT	DOMAIN	840	902	EGF-like 16.	OC
FT	DOMAIN	904	940	EGF-like 17, calcium-binding (Potential).	OC
FT	DOMAIN	942	978	EGF-like 18, calcium-binding (Potential).	OC
FT	DOMAIN	980	1021	EGF-like 19.	OX
FT	DOMAIN	1023	1205	Laminin G-like 1.	RN
FT	DOMAIN	1207	1243	EGF-like 20.	RP
FT	DOMAIN	1250	1480	Laminin G-like 2.	RX
FT	DOMAIN	1481	1517	EGF-like 21.	RA
FT	DOMAIN	1558	1758	Laminin G-like 3.	RA
FT	DOMAIN	1759	1795	EGF-like 22.	RA
FT	DOMAIN	1797	1833	EGF-like 23, calcium-binding (Potential).	RA
FT	DOMAIN	1835	1871	EGF-like 24, calcium-binding (Potential).	RA
FT	DOMAIN	1874	1915	EGF-like 25.	RA
FT	DOMAIN	1915	1951	EGF-like 26.	RA
FT	DOMAIN	1953	1989	EGF-like 27, calcium-binding (Potential).	RA
FT	DOMAIN	1991	2029	EGF-like 28, calcium-binding (Potential).	RA
FT	DOMAIN	2030	2070	EGF-like 29.	RA
FT	DISULFID	271	282	By similarity.	RA
FT	DISULFID	276	291	By similarity.	RA
FT	DISULFID	293	302	By similarity.	RA
FT	DISULFID	310	321	By similarity.	RA
FT	DISULFID	315	331	By similarity.	RA
FT	DISULFID	332	342	By similarity.	RA
FT	DISULFID	352	363	By similarity.	RA
FT	DISULFID	357	374	By similarity.	RA
FT	DISULFID	376	385	By similarity.	RA
FT	DISULFID	392	403	By similarity.	RA
FT	DISULFID	397	412	By similarity.	RA
FT	DISULFID	414	424	By similarity.	RA
FT	DISULFID	431	442	By similarity.	RA
FT	DISULFID	436	451	By similarity.	RA
FT	DISULFID	453	462	By similarity.	RA
FT	DISULFID	468	479	By similarity.	RA
FT	DISULFID	473	488	By similarity.	RA
FT	DISULFID	490	499	By similarity.	RA
FT	DISULFID	505	515	By similarity.	RA
FT	DISULFID	509	520	By similarity.	RA
FT	DISULFID	522	531	By similarity.	RA
FT	DISULFID	549	562	By similarity.	RA
FT	DISULFID	556	569	By similarity.	RA
FT	DISULFID	571	580	By similarity.	RA
FT	DISULFID	586	597	By similarity.	RA
FT	DISULFID	591	602	By similarity.	RA
FT	DISULFID	604	610	By similarity.	RA
FT	DISULFID	613	624	By similarity.	RA
FT	DISULFID	618	634	By similarity.	RA
FT	DISULFID	636	645	By similarity.	RA
FT	DISULFID	652	664	By similarity.	RA
FT	DISULFID	659	673	By similarity.	RA
FT	DISULFID	675	684	By similarity.	RA
FT	DISULFID	691	702	By similarity.	RA
FT	DISULFID	696	711	By similarity.	RA
FT	DISULFID	713	722	By similarity.	RA
Query Match					55.8%; Score 67; DB 1; Length 2139;
Best Local Similarity					28.0%; Pred. No. 2.8e+02;
Matches					7; Conservative 13; Mismatches 5; Indels 0; Gaps 0;
QY	2 XINXOCXOXLDCCSXKNXNXC 26				
DB	1826 GFEGHCEQNIDECQPCHNGNC 1850				
RESULT 15					
Q9VC97	PRELIMINARY; PRT; 2146 AA.				
AC	Q9VC97;				
DT	01-MAY-2000 (TrEMBLrel. 13, Created)				
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	CG6383-PA.				
GN	Name=crb; ORFNames=CG6383;				
OS	Drosophila melanogaster (fruit fly).				

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; OC Ephydroidea; Drosophilidae; Drosophila. X
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Borchan M.R., Bouck J., Brokstein P., Brotter P., RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Merkulo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J., RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O., RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R., RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R., RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,


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RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Obha H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268(2003).
DR EMBL; AB100603; BAC77038.1; -.
DR HSSP; P07207; IOT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0030152; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR00152; Asx hydroxyl S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00179; EGF_Ca; 25.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 35.
DR PROSITE; PS01187; EGF_Ca; 21.
KW ANK repeat; EGF-like domain; Receptor; Transmembrane.
SQ SEQUENCE 2516 AA; 269177 MW; 17FD72740EBD6E35 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2516;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXXNKCVCV 27
Db 233 GFAGQNCENVDPCGNNCKNGACV 259

RESULT 18
Q7TQ51
ID Q7TQ51 PRELIMINARY; PRT; 2536 AA.
AC Q7TQ51;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1 D.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=22753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Obha H., Ukai H., Katsube T., Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268(2003).
DR EMBL; AB100603; BAC77039.1; -.
DR HSSP; P07207; IOT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.

```

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DR InterPro; IPR002110; ANK.
DR InterPro; IPR00152; Asx hydroxyl S.
DR InterPro; IPR00742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF_Ca; 4.
DR Pfam; PF00066; Notch; 3.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_Ca; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS0010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_Ca; 21.
KW ANK repeat; EGF-like domain; Receptor; Transmembrane.
SQ SEQUENCE 2526 AA; 270583 MW; 017563FCE9703264 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2526;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSXXCNXXNKCVCV 27
Db 243 GFAGQNCENVDPCGNNCKNGACV 268

RESULT 19
NTCL MOUSE
ID NTCL_MOUSE STANDARD; PRT; 2531 AA.
AC Q01705; Q06007; Q61905; Q99JC2; Q9QW58; Q9R0X7;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)
DE (mtl4) (p300).
GN Name=Notch1; Synonyms=Notch;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Embryo;
RX MEDLINE=93194170; PubMed=849489;
RA Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,
RA Copeland N.G., Gridley T.;
RT "Cloning, analysis, and chromosomal localization of Notch-1, a mouse
RT homolog of Drosophila Notch.";
RL Genomics 15:259-264(1993).
RN [2]
RP SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.
RC STRAIN=CD-1; TISSUE=Embryo;
RX MEDLINE=93050801; PubMed=1426644;
RA Reaume A.G., Conlon R.A., Ziringibl R., Yamaguchi T.P., Rossant J.;
RT "Expression analysis of a Notch homologue in the mouse embryo.";
RL Dev. Biol. 154:377-387(1992).
RN [3]
RP SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.
RC TISSUE=Embryo;
RX MEDLINE=93048835; PubMed=1425352;
RA Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,
RA Greenspan R.J., McMahon A.P., Gridley T.;
RT "Expression pattern of Notch, a mouse homolog of Drosophila Notch,
RT suggests an important role in early postimplantation mouse
RT development.";
RL Development 115:737-744(1992).
RN [4]

```

RP SEQUENCE OF 1161-1547 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
RX MEDLINE=93178563; PubMed=8440332; DOI=10.1006/excr.1993.1044;
RA Lardelli M., Lendahl U.;
RT "Mottch A. and Mottch B-two mouse Notch homologues coexpressed in a wide
variety of tissues.";
RL Exp. Cell Res. 204:364-372(1993).
RN [5]
RP SEQUENCE OF 1659-1673 FROM N.A.
RX MEDLINE=99364499; PubMed=10437788; DOI=10.1016/S0014-5793(99)00901-1;
RA Lee J.S., Ishimoto A., Yanagawa S.I.;
RT "Murine leukemia provirus-mediated activation of the Notch1 gene leads
to induction of HES-1 in a mouse T lymphoma cell line, DL-3.";
RL FEBS Lett. 455:276-280(1999).
RN [6]
RP SEQUENCE OF 1950-2201 FROM N.A.
RX MEDLINE=98029496; PubMed=9384671;
RA Messerle M., Follo M., Nehls M., Eggert H., Boehm T.;
RT "Dynamic changes in gene expression during in vitro differentiation of
mouse embryonic stem cells.";
RL Cytokines Cell. Mol. Ther. 1:139-143(1995).
RN [7]
RP SEQUENCE OF 1655-1659, CLEAVAGE BY FURIN-LIKE CONVERTASE, AND
MUTAGENESIS OF 1651-ARG--ARG-1654.
RX MEDLINE=98318619; PubMed=9653148; DOI=10.1073/pnas.95.14.8108;
RA Isgrat F., Bessia C., Brou C., LeBail O., Jarriault S., Seidah N.G.,
RA Israel A.;
RT "The Notch1 receptor is cleaved constitutively by a furin-like
convertase.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8108-8112(1998).
RN [8]
RP SEQUENCE OF 1865-2075 FROM N.A., AND DEVELOPMENTAL STAGE IN HAIR
FOLLICLES.
RX PubMed=8486742; DOI=10.1083/jcb.121.3.631;
RA Kopan R., Weintraub H.;
RT "Mouse notch: expression in hair follicles correlates with cell fate
determination.";
RL J. Cell Biol. 121:631-641(1993).
RN [9]
RP PARTIAL SEQUENCE, AND POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
RT "Murine notch homologs (N1-4) undergo presenilin-dependent
proteolysis.";
RL J. Biol. Chem. 276:40268-40273(2001).
RN [10]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
RN [11]
RP INTERACTION WITH DTX1 AND DTX2.
RX MEDLINE=21123790; PubMed=11226752; DOI=10.1016/S0736-5748(00)00071-X;
RA Kishi N., Tang Z., Maeda Y., Hirai A., Mo R., Ito M., Suzuki S.,
RA Nakao K., Kinoshita T., Kadesch T., Hui C.-C., Artavanis-Tsakonas S.,
RA Okano H., Matsuno K.;
RT "Murine homologs of Deltex define a novel gene family involved in
vertebrate Notch signaling and neurogenesis.";
RL Int. J. Dev. Neurosci. 19:21-35(2001).
RN [12]
RP FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (By similarity). May play an essential role in
postimplantation development, probably in some aspect of cell
specification and/or differentiation. May be involved in mesoderm
development, somit formation and neurogenesis. Involved in the
maturation of both CD4+ and CD8+ cells in the thymus. Important
for follicular differentiation and possibly cell fate selection

CC within the follicle.
CC -! SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds. Interacts with DTX1 and DTX2.
CC -! SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
CC -! ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoID=Q01705-1; Sequences=Displayed;
CC Name=2;
CC IsoID=Q01705-2; Sequence=VSP_001402, VSP_001403, VSP_001404;
CC Note=No experimental confirmation available;
CC TISSUE SPECIFICITY: Highly expressed in the brain, lung and
thymus. Expressed at lower levels in the spleen, bone-marrow,
spinal cord, eyes, mammary gland, liver, intestine, skeletal
muscle, kidney and heart. In the hair follicle, highly expressed
exclusively in the epithelial compartment.
CC DEVELOPMENTAL STAGE: First detected in the mesoderm at 7.5 dpc By
8.5 dpc highly expressed in presomitic mesoderm, mesenchyme and
endothelial cells, while much lower levels are seen in the
neuroepithelium. Between 9.5-10.5 dpc expressed at high levels in
the neuroepithelium. At 13.5 dpc expressed in the surface
ectoderm, eye and developing whisker follicles. Hair follicle
matrix cells expression starts as different cell types become
distinguishable in the developing follicle. Expression persists
throughout the growth phase of the follicle and maintains the same
expression profile in the second hair cycle. The cells in the
follicle that undergo a phase of high level expression are in
transition from mitotic precursors to several discreet,
differentiating cell types.
CC -! PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(EC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane.
CC -! PTM: Phosphorylated.
CC -! SIMILARITY: Belongs to the NOTCH family.
CC -! SIMILARITY: Contains 5 ANK repeats.
CC -! SIMILARITY: Contains 36 EGF-like domains.
CC -! SIMILARITY: Contains 3 Lin/Notch repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z11886; CAA77941.1; -
CC EMBL; L02613; AAK14898.1; -
CC EMBL; X68278; CAA48339.1; -
CC EMBL; AJ238029; CAB40733.1; -
CC EMBL; X82562; CAA57909.1; -
CC PIR; A46019; A46019.
CC PIR; B49175; B49175.
CC HSSP; P46531; 1PB5.
CC MGD; MGI-97363; Notch1.
CC GO; GO:0005887; C:integral to plasma membrane; IC.
CC GO; GO:0005515; F:protein binding; IFI.
CC GO; GO:0030154; P:cell differentiation; IMP.
CC GO; GO:0007386; P:compartment specification; IMP.
CC GO; GO:0007368; P:determination of left/right symmetry; IMP.
CC GO; GO:0007219; P:Notch signaling pathway; IC.
CC GO; GO:0045944; P:positive regulation of transcription from P. .; IDA.
CC GO; GO:0048103; P:somatic stem cell renewal; IDA.

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DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_III.
DR InterPro; IPR010660; NOD.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 7.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF06816; NOD; 1.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.

Query Match 55.8%; Score 67; DB 1; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXCXOXLDCCSXXCNXXNVCV 27
Db 248 GFAGQNCENVDCCPGNCKNGGACV 273

RESULT 20
NTCl RAT
ID NTCl RAT STANDARD; PRT; 2531 AA.
AC Q07008;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1).
GN Name=Notch1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Schwann cell;
RX MEDLINE=92111383; PubMed=1764995;
RA Weinmaster G., Roberts V.J., Lemke G.;
RT "A homolog of Drosophila Notch expressed during mammalian
RL development.";
RL Development 113:199-205 (1991).
RN [2]
RP REVISIONS TO 1652-1653.
RA Weinmaster G.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP FUNCTION.
RX MEDLINE=21094508; PubMed=11182080; DOI=10.1016/S0896-6273(01)00179-9;
RA Tanigaki K., Nogaki F., Takahashi J., Tashiro K., Kurooka H.,
RA Honjo T.;
RT "Notch1 and Notch3 instructively restrict bcrf-responsive multipotent
RT neural progenitor cells to an astroglial fate.";
RL Neuron 29:45-55 (2001).
RN [4]
RP TISSUE SPECIFICITY.
RX MEDLINE=93202015; PubMed=1295745;
RA Weinmaster G., Roberts V.J., Lemke G.;
RT "Notch2: a second mammalian Notch gene.";
RL Development 116:931-941 (1992).
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=21331789; PubMed=11438922; DOI=10.1002/cne.1059.abs;
RA Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple
RT functional roles for the Notch-DSL signaling system during brain
RT development.";
RL J. Comp. Neurol. 436:167-181 (2001).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands

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CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). Acts instructively to control
CC the cell fate determination of CNS multipotent progenitor cells,
CC resulting in astroglial induction and neuron/oligodendrocyte
CC suppression.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Expressed in the brain, kidney and spleen.
CC Expressed in postnatal central nervous system (CNS) germinal zones
CC and, in early postnatal life, within numerous cells throughout the
CC CNS. Found in both subventricular and ventricular germinal zones.
CC -!- DEVELOPMENTAL STAGE: In the embryo, highest levels occur between
CC days 12 and 14 and decrease rapidly to much lower levels in the
CC adult.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane (By similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 5 ANK repeats.
CC -!- SIMILARITY: Contains 36 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.

```

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/
or send an email to license@sib-sib.ch).
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EMBL; X57405; CAA40667.1; -.
HSSP; P46531; 1PB5.
RGD; 3187; Notch1.
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_III.
InterPro; IPR010660; NOD.
InterPro; IPR008297; Notch.
InterPro; IPR000800; Notch_region.
Pfam; PF00023; Ank; 6.
Pfam; PF00008; EGF; 35.
Pfam; PF06816; NOD; 1.
Pfam; PF00066; Notch; 3.
PIRSF; PIRSF002279; Notch; 1.
PRINTS; PR01415; ANKYRIN.
PRINTS; PR00010; EGF_BLOOD.
PRINTS; PR01452; NOTCH.
SMART; SM00248; ANK; 6.
SMART; SM00179; EGF_CA; 25.
SMART; SM00004; NL; 3.
PROSITE; PS50297; ANK_REPEAT_REGION; 1.
PROSITE; PS50088; ANK_REPEAT; 4.
PROSITE; PS00010; ASX_HYDROXYL; 22.

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Query Match	55.8%	Score 67	DB 1	Length 2531
Best Local Similarity	30.8%	Pred No. 3.2e+02		
Matches	8	Conservative 12	Mismatches 6	Indels 0
Gaps	0			
FT DISULFID	106	117	By similarity.	
FT DISULFID	111	127	By similarity.	
FT DISULFID	129	138	By similarity.	
FT DISULFID	144	155	By similarity.	
FT DISULFID	149	164	By similarity.	
FT DISULFID	166	175	By similarity.	
FT DISULFID	182	195	By similarity.	
FT DISULFID	189	204	By similarity.	
Qy	2	XIXNQXQXQXLDCCSCXCNXXNXCVC	27	
Db	248	GFAGQNCENVDVDCPNNGCKGACVC	273	
RESULT 21				
Q8K428				
ID	Q8K428	PRELIMINARY	PRT	2531 AA
AC	Q8K428			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Notch 1 protein.			
GN	Name=Notch1			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Thymus;			
RA	Medline=95044925; PubMed=7956822;			
RA	Nye J.S., Kopan R., Axel R.;			
RT	"An activated Notch suppresses neurogenesis and myogenesis but not gliogenesis in mammalian cells."			
RL	Development 120:2421-2430(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Thymus;			
RA	Medline=21119593; PubMed=12123574; DOI=10.1016/S0960-9822(02)00888-6;			
RA	Foltz D.R., Santiago M.C., Berechid B.E., Nye J.S.;			
RT	"Glycogen synthase kinase-3beta modulates notch signaling and stability."			
RL	Curr. Biol. 12:1006-1011(2002).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/c; TISSUE=Thymus;			
RA	Schellin K.A., Pauley A.M., Nye J.S.;			
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF508809; AAM28905.1; ..			
DR	PIR; A46438; A46438.			
DR	HSSP; P46531; LPB5.			
DR	MGD; MGI:97363; Notch1.			
DR	GO; GO:0005515; C:extracellular space; TAS.			
DR	GO; GO:0005515; P:protein binding; IPI.			
DR	GO; GO:0001708; P:cell fate specification; IMP.			
DR	GO; GO:0007386; P:compartment specification; IMP.			
DR	GO; GO:0007368; P:determination of left/right symmetry; IMP.			
DR	GO; GO:0007492; P:endoderm development; IMP.			
DR	GO; GO:0001837; P:epithelial to mesenchymal transition; IMP.			
DR	GO; GO:0007507; P:heart development; IMP.			
DR	GO; GO:0030215; P:keratinocyte differentiation; IMP.			
DR	GO; GO:0007219; P:Notch signaling pathway; IMP.			
DR	GO; GO:0043065; P:positive regulation of apoptosis; IDA.			
DR	GO; GO:0045944; P:positive regulation of transcription from P. . .; IDA.			
DR	GO; GO:0048103; P:somatic stem cell division; IDA.			
DR	InterPro; IPR002110; ANK.			
DR	InterPro; IPR000152; ANK_hydroxyl_S.			
DR	InterPro; IPR000742; EGF 2.			
DR	InterPro; IPR001881; EGF Ca.			

DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR008000; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 30.
DR Pfam; PF07645; EGF_CA; 5.
DR Pfam; PF00666; Notch; 3.
DR FIRSF; FIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFBLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_CA; 21.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 70819 MW; 7DBE7DEDF799D999 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DQ 2 XIXNQXCXXQLDDCCSXCNXXNKCVCV 27
Db 248 GFAGNCENVDPCGNCKNGGACV 273

RESULT 22

ID Q7TQ50 PRELIMINARY; PRT; 2531 AA.

AC Q7TQ50;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=2753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Onba H., Ukai H., Katsube T., Ogiu T.;
RA "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268 (2003).
DR DR
DR EMBL; AB106603; BAC77040.1; -.
DR HSSP; P07207; 1OT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF07645; EGF_CA; 4.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_CA; 21.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 70819 MW; 7DBE7DEDF799D999 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DQ 2 XIXNQXCXXQLDDCCSXCNXXNKCVCV 27
Db 248 GFAGNCENVDPCGNCKNGGACV 273

RESULT 22

ID Q7TQ50 PRELIMINARY; PRT; 2531 AA.

AC Q7TQ50;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=2753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Onba H., Ukai H., Katsube T., Ogiu T.;
RA "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268 (2003).
DR DR
DR EMBL; AB106603; BAC77040.1; -.
DR HSSP; P07207; 1OT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF07645; EGF_CA; 4.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_CA; 21.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 70819 MW; 7DBE7DEDF799D999 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DQ 2 XIXNQXCXXQLDDCCSXCNXXNKCVCV 27
Db 248 GFAGNCENVDPCGNCKNGGACV 273

RESULT 22

ID Q7TQ50 PRELIMINARY; PRT; 2531 AA.

AC Q7TQ50;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transmembrane receptor Notch1.
GN Name=Notch1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RX MEDLINE=2753192; PubMed=12807718; DOI=10.1093/carcin/bgg071;
RA Tsuji H., Ishii-Onba H., Ukai H., Katsube T., Ogiu T.;
RA "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphoma.";
RL Carcinogenesis 24:1257-1268 (2003).
DR DR
DR EMBL; AB106603; BAC77040.1; -.
DR HSSP; P07207; 1OT8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF07645; EGF_CA; 4.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 25.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS00026; EGF_3; 36.
DR PROSITE; PS01187; EGF_CA; 21.
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 70819 MW; 7DBE7DEDF799D999 CRC64;

Query Match 55.8%; Score 67; DB 2; Length 2531;
Best Local Similarity 30.8%; Pred. No. 3.2e+02;
Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

DQ 2 XIXNQXCXXQLDDCCSXCNXXNKCVCV 27
Db 248 GFAGNCENVDPCGNCKNGGACV 273

RESULT

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RESULT 24
Q91902 PRELIMINARY; PRT; 721 AA.
AC Q91902;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE X-Delta-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Anopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319507; PubMed=7596411; DOI=10.1038/375787a0;
RA Henrique D., Adam J., Myat A., Chitnis A., Lewis J., Ish-Horowitz D.;
RT "Expression of a Delta homologue in prospective neurons in the
RT chick.";
RL Nature 375:787-790(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319503; PubMed=7596407; DOI=10.1038/375761a0;
RA Chitnis A., Henrique D., Lewis J., Ish-Horowitz D., Kintner C.;
RT "Primary neurogenesis in Xenopus embryos regulated by a homologue of
RT the Drosophila neurogenic gene Delta.";
RL Nature 375:761-766(1995).
DR EMBL; L42229; AAC38017.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 721 AA; 79922 MW; 9EBDC85C439DD194 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 721;
Best Local Similarity 32.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXQLDCCSXGXNXXNC 26
Db 436 GFSGRNCDNLDCTSFPCQNGTC 460

RESULT 25
Q61Q50 PRELIMINARY; PRT; 1317 AA.
AC Q61Q50;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE NOTCH2 protein (Fragment).
GN Name=NOTCH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 28 EGF-like domains.
DR EMBL; BC071562; AAH71562.1; -.
DR HSSP; P00743; 1APO.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_5.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 22.
DR Pfam; PF07645; EGF_CA; 5.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM00181; EGF; 31.
DR SMART; SM00179; EGF_CA; 30.
DR PROSITE; PS00010; ASX HYDROXYL; 21.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS00026; EGF_3; 31.
DR PROSITE; PS01187; EGF_CA; 21.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1317 AA; 140756 MW; 1A2674F4AF001646 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 1317;
Best Local Similarity 25.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN----QXCXQLDCCSXGXNXXNCV 27
Db 406 CVCVNGSGDDCSNIDDCAFASCTPGSTCI 436

RESULT 26
Q9NGV4 PRELIMINARY; PRT; 1551 AA.
ID Q9NGV4
AC Q9NGV4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SP1070.
GN Name=SP1070;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

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DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; Ank; 6.
DR Pfam; PF00008; EGF; 32.
DR Pfam; PF07645; EGF_CA; 3.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 22.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 35.
DR PROSITE; PS01186; EGF_2; 29.
DR PROSITE; PS00026; EGF_3; 35.
DR PROSITE; PS01187; EGF_CA; 20.
KW ANK repeat; EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 2447 AA; 26252 MW; 1ABE2A372A085D84 CRC64;

Query Match 55.0%; Score 66; DB 2: Length 2447;
Best Local Similarity 29.0%; Pred. No. 3.9e+02;
Matches 9; Conservative 15; Mismatches 3; Indels 4; Gaps

QY 1 CXTYN-----QXCXQKLDCCSXKCNXXKCV 27
   |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
DB 279 CVCVNGWSGLDCSENIDCDTAACSPGTCV 309

RESULT 28
NTC2 MOUSE STANDARD; PRT; 2470 AA.
AC Q35516; Q06008; Q60941;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Notch
DE B).
GN Name=Notch2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP RP
RC STRAIN=C57BL/6; TISSUE=Thymus;
RC Hamada Y., Higuchi M., Tsujimoto Y.;
RT "Complete amino acid sequence and multiform transcripts encoded by a
RT single copy of mouse Notch2 gene.";
RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP RP
RC SEQUENCE OF 316-1518 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
RC MEDLINE=93178563; PubMed=8440332; DOI=10.1006/excr.1993.1044;
RA Lardelli M., Lendahl U.;
RT "Notch A and Notch B-two mouse Notch homologues coexpressed in a wide
RT variety of tissues.";
RN [3]
RP RP
RC Exp. Cell Res. 204:364-372 (1993).
RP RP
RP SEQUENCE OF 1765-2153 FROM N.A.
RP MEDLINE=97075110; PubMed=8917536; DOI=10.1073/pnas.93.23.13014;
RA Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
RA Martin D.I.;
RT "Inhibition of granulocytic differentiation by mNotch1.";
RN [4]
RP RP
RC Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019 (1996).
RP RP
RP FUNCTION
RP MEDLINE=99396706; PubMed=10393120;
RA Hamada Y., Kadokawa Y., Okabe M., Ikawa M., Coleman J.R.

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RA Tsubamoto Y.; "Mutation in ankyrin repeats of the mouse Notch2 gene induces early embryonic lethality.";
 RL Development 126:3415-3424 (1999).
 [5]
 RP DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
 RA MEDLINE=95333893; PubMed=7609614; DOI=10.1016/0169-328X(94)00257-F;
 RX Higuchi M., Kiyama H., Hayakawa T., Hamada Y., Tsubamoto Y.;
 RA "Differential expression of Notch1 and Notch2 in developing and adult mouse brain.";
 RL Brain Res. Mol. Brain Res. 29:263-272 (1995).
 [6]
 RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
 RX Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
 RA "Murtine notch homologs (N1-4) undergo presenilin-dependent proteolysis.";
 RL J. Biol. Chem. 276:40268-40273 (2001).
 [7]
 RP POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
 RX MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction among mammalian Notch family members.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).
 CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation.
 CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O35516-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O35516-2; Sequence=VSP_001405;
 CC Note=No experimental confirmation available;
 CC TISSUE SPECIFICITY: Expressed in the brain, liver, kidney, neuroepithelia, somites, optic vesicles and branchial arches, but not heart.
 CC -I- DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone, the postnatal ependymal cells, and the choroid plexus throughout embryonic and postnatal development.
 CC -I- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane.
 CC -I- PTM: Phosphorylated.
 CC -I- SIMILARITY: Belongs to the NOTCH family.
 CC -I- SIMILARITY: Contains 6 ANK repeats.
 CC -I- SIMILARITY: Contains 35 EGF-like domains.
 CC -I- SIMILARITY: Contains 2 Lin/Notch repeats.
 CC -----
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 CC -----
 DR EMBL: D32210; BAA22094.1; -
 DR EMBL: X68279; CAA48340.1; -
 DR EMBL: U51881; AAC52924.1; -
 DR FIRM: A49175; A49175.
 DR HSSP: Q9UCV4; INZI.
 DR MGI: 97364; Notch2.
 DR GO: GO:0009986; C:cell surface; ISS.
 DR GO: GO:0005887; C:integral to plasma membrane; IC.
 DR GO: GO:0005634; C:nucleus; IDA.
 DR GO: GO:0003706; F:ligand-regulated transcription factor activity; ISS.
 DR GO: GO:000515; F:protein binding; IPT.
 DR GO: GO:0006916; P:anti-apoptosis; ISS.
 DR GO: GO:0007050; P:cell cycle arrest; ISS.
 DR GO: GO:0001709; P:cell fate determination; TAS.
 DR GO: GO:0016049; P:cell growth; ISS.
 DR GO: GO:0007368; P:determination of left/right symmetry; IMP.
 DR GO: GO:0007275; P:development; ISS.
 DR GO: GO:0030097; P:hemopoiesis; ISS.
 DR GO: GO:0006917; P:induction of apoptosis; ISS.
 DR GO: GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
 DR GO: GO:0008285; P:negative regulation of cell proliferation; ISS.
 DR GO: GO:0007219; P:Notch signaling pathway; IC.
 DR GO: GO:0046579; P:positive regulation of RAS protein signal t...; ISS.
 DR GO: GO:0042060; P:wound healing; IDA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR000152; ASX_hydroxyl_S.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_CA.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR010660; NOD.
 DR InterPro: IPR008297; Notch.
 DR InterPro: IPR008000; Notch_region.
 DR Pfam: PF00023; Ank; 6.
 DR Pfam: PF00008; EGF; 34.
 DR Pfam: PF06816; NOD; 1.
 DR Pfam: PF00066; Notch; 2.
 DR Pfam: PF002279; Notch; 1.
 DR PRINTS: PR01415; ANKYRIN.
 DR PRINTS: PR00010; EGFBLD.
 DR PRINTS: PR01452; NOTCH.
 DR SMART: SM00248; ANK; 6.
 DR SMART: SM00179; EGF_CA; 23.
 DR SMART: SM00004; NL; 3.
 DR PROSITE: PS0297; ANK_REPEAT; 1.
 DR PROSITE: PS00088; ANK_REPEAT; 4.
 DR PROSITE: PS00010; ASX_HYDROXYL; 22.
 DR PROSITE: PS00022; EGF_1; 33.
 DR PROSITE: PS01386; EGF_2; 27.
 DR PROSITE: PS00026; EGF_3; 35.
 DR PROSITE: PS01187; EGF_CA; 22.
 KW Activator; Alternative splicing; ANK repeat; Developmental protein; Differentiation; EGF-like domain; Glycoprotein; Notch signaling pathway; Phosphorylation; Receptor; Repeat; Signal; Transcription regulation; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 2470 Neurogenic locus notch homolog protein 2.
 FT CHAIN 1666 2470 Notch extracellular truncation.
 FT CHAIN 1697 2470 Notch intracellular domain.
 FT DOMAIN 26 1677 Extracellular (Potential).
 FT TRANSMEM 1678 1698 Potential.
 FT DOMAIN 1699 2470 Cytoplasmic (Potential).
 FT DOMAIN 26 63 EGF-like 1.
 FT DOMAIN 64 102 EGF-like 2.
 FT DOMAIN 105 143 EGF-like 3.
 FT DOMAIN 144 180 EGF-like 4.
 FT DOMAIN 182 219 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN 221 256 EGF-like 6 (incomplete).

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FT DOMAIN 258 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 296 EGF-like 8, calcium-binding (Potential).
FT DOMAIN 336 EGF-like 9, calcium-binding (Potential).
FT DOMAIN 373 EGF-like 10, calcium-binding (Potential).
FT DOMAIN 413 EGF-like 11, calcium-binding (Potential).
FT DOMAIN 454 EGF-like 12, calcium-binding (Potential).
FT DOMAIN 492 EGF-like 13, calcium-binding (Potential).
FT DOMAIN 530 EGF-like 14, calcium-binding (Potential).
FT DOMAIN 568 EGF-like 15, calcium-binding (Potential).
FT DOMAIN 605 EGF-like 16, calcium-binding (Potential).
FT DOMAIN 643 EGF-like 17, calcium-binding (Potential).
FT DOMAIN 680 EGF-like 18, calcium-binding (Potential).
FT DOMAIN 718 EGF-like 19, calcium-binding (Potential).
FT DOMAIN 755 EGF-like 20, calcium-binding (Potential).
FT DOMAIN 793 EGF-like 21, calcium-binding (Potential).
FT DOMAIN 831 EGF-like 22, calcium-binding (Potential).

Query Match 55.0%; Score 66; DB 1; Length 2470;
Best Local Similarity 25.8%; Pred. No. 3.9e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps 1;

QY 1 CXIXN---QXQXLDCCSXCNXXNKCXV 27
Db 322 CVCVNGSGDDCSENIDDCVASCIPGSGTCI 352

RESULT 29
NTC2 HUMAN STANDARD; PRT; 2471 AA.
AC Q04721; Q99734; Q9H240;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2).
GN Name=NOTCH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Blaumeueller C.M., Mann R.S.;
RT "Complete human notch 2 (hN2) cDNA sequence.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.G.;
RT "Human Notch2, a novel member of cell-fate determining NOTCH family.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 967-1229 FROM N.A.
RC TISSUE=T-cell;
RA Lemasson I., Devaux C., Mesnard J.M.;
RT "Partial sequence of EGF-like repeat domain of human Notch2 mRNA.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1810-2447 FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=93265135; PubMed=1303260;
RA Scifani S., Blaumeueller C.M., Redhead N.J., Hill R.E.,
RA Artavanis-Tsakonas S.;
RT "Human homologs of a Drosophila enhancer of split gene product define
a novel family of nuclear proteins.";
RL Nat. Genet. 2:119-127(1992).
RN [5]
RP POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=97386453; PubMed=9244302; DOI=10.1016/S0092-8674(00)80336-0;
RA Blaumeueller C.M., Qi H., Zagouras P., Artavanis-Tsakonas S.;
RT "Intracellular cleavage of Notch leads to a heterodimeric receptor on
the plasma membrane.";
RL Cell 90:281-291(1997).

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RN [6]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
RT "Human ligands of the Notch receptor.";
RL Am. J. Pathol. 154:785-794(1999).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity).
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus.
CC -!- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung,
CC skeletal muscle and liver.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane (By similarity).
CC -!- PTM: Phosphorylated (By similarity).
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 6 ANK repeats.
CC -!- SIMILARITY: Contains 35 EGF-like domains.
CC -!- SIMILARITY: Contains 2 Lin/Notch repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF308601; AAA36377.2; -
DR EMBL; AF315356; AAG37073.1; -
DR EMBL; U77493; AAB19224.1; -
DR HSSP; P00740; 1EDM.
DR Genew; HGNC:7882; NOTCH2.
DR MIM; 600275; -
DR GO; GO:0009986; C:cell surface; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003706; F:ligand-regulated transcription factor activity; TAS.
DR GO; GO:0005515; F:protein binding; NAS.
DR GO; GO:0046982; F:protein heterodimerization activity; NAS.
DR GO; GO:0004872; F:receptor activity; NAS.
DR GO; GO:0006916; P:anti-apoptosis; TAS.
DR GO; GO:0007050; P:cell cycle arrest; IDA.
DR GO; GO:0001709; P:cell fate determination; TAS.
DR GO; GO:0016049; P:cell growth; IDA.
DR GO; GO:0007368; P:determination of left/right symmetry; ISS.
DR GO; GO:0030097; P:hemopoiesis; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0002011; P:morphogenesis of an epithelial sheet; ISS.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR GO; GO:0007399; P:neurogenesis; NAS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0046579; P:positive regulation of RAS protein signal t...; IDA.
DR GO; GO:0019827; P:stem cell maintenance; TAS.
DR InterPro; IPR002110; ANK.

```

FT	DOMAIN	1374	1412	EGF-like 35.
FT	REPEAT	1420	1456	Lin/Notch 1.
FT	REPEAT	1503	1535	Lin/Notch 2.
FT	REPEAT	1827	1871	ANK 1.
FT	REPEAT	1876	1905	ANK 2.
FT	REPEAT	1909	1939	ANK 3.
FT	REPEAT	1943	1972	ANK 4.
FT	REPEAT	1976	2005	ANK 5.
FT	REPEAT	2009	2038	ANK 6.

Query Match 55.0%; Score 66; DB 1; Length 2471;
Best Local Similarity 25.8%; Pred. No. 4e+02;
Matches 8; Conservative 14; Mismatches 5; Indels 4; Gaps

Qy	1	324	354
Qy	1	324	354
Db	1	324	354

RESULT 30

ID	NTC2 RAT	STANDARD;	PRT;	2471 AA.
AC	OSQW10;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Neurogenic locus notch homolog protein 2 precursor (Notch 2).			
GN	Names=Notch2;			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OC	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=93202015; PubMed=1295745;			
RA	Weinmaster G., Roberts V.J., Lemke G.;			
RT	"Notch2: a second mammalian Notch gene.";			
RL	Development 116:931-941(1992).			
RN	[2]			
RP	TISSUE SPECIFICITY.			
RX	MEDLINE=21331789; PubMed=11439922; DOI=10.1002/cne.1059.abs;			
RA	Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;			
RT	"Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development.";			
RL	J. Comp. Neurol. 436:167-181(2001).			
CC	-1- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).			
CC	-1- SUBUNIT: Heterodimer of a C-terminal fragment N(TW) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.			
CC	-1- TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and kidney.			
CC	-1- DEVELOPMENTAL STAGE: Expressed in the brain during E14 and E17.			
CC	-1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TW) and a N-terminal fragment N(EC). Following			

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CG9138-PA.
GN Names=SP1070; ORFNames=CG9138;
OS Drosophila melanogaster [Fruit fly].
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hartis N.L., Harvey D., Heian T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodagat, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 2 F5/8 type C domains.
DR EMBL: AE003615; AAF52472.1; -.
DR HSSP: P00740; 1EDM.
DR FlyBase: FBgn0031879; SP1070.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR GO: GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR000152; Asx hydroxyl S.
DR InterPro: IPR008985; ConA_like lec_gl.
DR InterPro: IPR000859; CUB_1-like.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_CA.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR000421; FAS8_C.
DR InterPro: IPR008979; Gal_bind-like.
DR InterPro: IPR009030; Growth_fac_recept.
DR InterPro: IPR003410; Hyalin.
DR InterPro: IPR002172; LDL_receptor_A.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR InterPro: IPR001368; TNFR_C6.
DR InterPro: IPR003129; TSP_N.
DR Pfam: PF00431; CUB; 3.
DR Pfam: PF00008; EGF; 12.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF02494; HVR; 3.
DR Pfam: PF02210; Laminin_G_2; 1.
DR Pfam: PF00057; Ldl_recept_a; 1.
DR PRINTS: PR00010; EGF_BLOOD.
DR SMART: SM00032; CCP; 8.
DR SMART: SM00042; CUB; 3.
DR SMART: SM00179; EGF_CA; 9.
DR SMART: SM00231; FAS8C; 2.
DR SMART: SM00192; LDLA; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00010; ASX_HYDROXYL; 11.
DR PROSITE: PS01180; CUB; 3.
DR PROSITE: PS00022; EGF_1; 15.
DR PROSITE: PS01186; EGF_2; 13.
DR PROSITE: PS00026; EGF_3; 16.
DR PROSITE: PS01187; EGF_CA; 7.
DR PROSITE: PS01285; FAS8C_1; UNKNOWN_1.
DR PROSITE: PS00022; FAS8C_3; 2.
DR PROSITE: PS00825; HVR; 3.
DR PROSITE: PS01209; LDLA_1; 1.
DR PROSITE: PS00068; LDLA_2; 1.
DR PROSITE: PS00923; SUSHI; 5.
KW EGF-like domain.
SQ SEQUENCE 3396 AA; 369389 MW; E618E9ACEA13E0E5 CRC64;

Query Match 55.0%; Score 66; DB 2; Length 3396;
Best Local Similarity 33.3%; Pred. No. 5.3e+02;

```
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
QY 4 XNQCXQXLDCCSXCNXXNCV 27
Db 2119 TGNQCHTIDDCASNPCQHGATCV 2142

RESULT 34
Q8AW87
ID Q8AW87 PRELIMINARY; PRT; 726 AA.
AC Q8AW87;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ligand Delta-1.
GN Name=Delta-1;
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
[1]
RN SEQUENCE FROM N.A.
RA Nakamura K., Kikuchi Y., Susaki K., Chiba C., Saito T.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AB095017; BAC41350.2; -.
DR HSSP; P00740; IEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR00152; ASX_HYDROXYL_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 17.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW EGF-like domain.
SQ SEQUENCE 726 AA; 79866 MW; 352A40219AB67F41 CRC64;

Query Match 54.2%; Score 65; DB 2; Length 726;
Best Local Similarity 32.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 2 XIXNQCXQXLDCCSXCNXXNCV 26
Db 437 GFGSRHCDENLDCCASYPGANGTC 461

RESULT 35
O42374
ID O42374 PRELIMINARY; PRT; 752 AA.
AC O42374;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch receptor protein (Fragment).
GN Name=notch2; Synonyms=Notch6;
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
```

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OX NCBI_TaxID=7955;
RN SEQUENCE FROM N.A.
RA Westin J., Lardelli M.;
RT "Three novel Notch genes in zebrafish: implications for vertebrate
RL Dev. Genes Evol. 207:51-63(1997).
DR EMBL; Y10354; CAA71380.1; -.
DR HSSP; P00740; IEDM.
DR ZFIN; ZDB-GENE-000329-4; notch2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR000152; ASX_HYDROXYL_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF07645; EGF_CA; 1.
DR Pfam; PF00066; Notch; 2.
DR PRINTS; PR00010; EGFBLD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00179; EGF_CA; 10.
DR SMART; SM00004; NL; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 9.
DR PROSITE; PS00022; EGF_1; 17.
DR PROSITE; PS01186; EGF_2; 15.
DR PROSITE; PS00026; EGF_3; 17.
DR PROSITE; PS01187; EGF_CA; 7.
KW EGF-like domain; Receptor.
FT NON_TER 1
FT NON_TER 752
SQ SEQUENCE 752 AA; 82103 MW; 30939E16B0327F8A CRC64;

Query Match 54.2%; Score 65; DB 2; Length 752;
Best Local Similarity 33.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;
QY 4 XNQCXQXLDCCSXCNXXNCV 27
Db 132 SGDNQCHTIDDCSNPCRNQGTVC 155

RESULT 36
Q9NC90
ID Q9NC90 PRELIMINARY; PRT; 1075 AA.
AC Q9NC90;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Scavenger receptor cysteine-rich protein variant 1.
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
[1]
RN SEQUENCE FROM N.A.
RA MEDLINE=20542095; PubMed=11069281; DOI=10.1073/pnas.230096397;
RA Pancer Z.;
RT "Dynamic expresion of multiple scavenger receptor cysteine-rich genes
RL in coelomocytes of the purple sea urchin."
Proc. Natl. Acad. Sci. U.S.A. 97:13156-13161(2000).
DR EMBL; AF228824; AAF76316.1; -.
DR HSSP; P00740; IEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR InterPro; IPR000152; ASX_HYDROXYL_S.
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nspr, pccool, lba,
GO; GO:0005059; P:calcium ion binding; IEA.
GO; GO:0005540; P:hyaluronic acid binding; IEA.
GO; GO:0005529; P:sugar binding; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro: IPR000152; Asx hydroxyl_S.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001861; EGF_Ca.
DR InterPro: IPR001438; EGF_II.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR003599; IG-like.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR000538; Link.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00008; EGF_2.
DR Pfam: PF00059; Lectin_C1.
DR Pfam: PF00084; Sushi_1.
DR Pfam: PF00193; Xlink_2.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR01265; LINKMODULE.
DR ProDom: PD000918; Link; 2.
DR SMART: SM00032; CCP; 1.
DR SMART: SM00034; CLECT; 1.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00445; LINK; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS0041; C_TYPE_LECTIN_2; 1.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
DR PROSITE: PS01241; LINK_1; 2.
DR PROSITE: PS00963; LINK_2; 2.
DR PROSITE: PS00923; SUSHI; 1.
DR EGF-like domain.
KW SEQUENCE 1230 AA; 139876 MW; 182BD86D0E40BE78 CRC64;

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Query Match          54.2%; Score 65; DB 2; Length 1290;
Best Local Similarity 26.9%; Pred. No. 2.8e+02;
Matches . 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNOXCXQXLDCCSXXCNXXNKCXV 27
DB 1005 GFTGENCEIDIDCLSSPQNGTCT 1030

RESULT 39
Q20204
ID Q20204 PRELIMINARY; . PRT; 1410 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein F4OE10.4.
GN Name=slt-1; ORFNames=F4OE10.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
RN [2];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smye R.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Smye R.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022270; CAB63434.2; -.
DR EMBL; Z69792; CAB63434.2; JOINED.
DR EMBL; AL022270; CAB93668.3; JOINED.
DR EMBL; Z69792; CAB93668.3; -.
DR PIR; D89711; D89711.
DR PIR; T22025; T22025.
DR HSSP; P00740; IEDM.
DR WormBase; WBGene00004854; slt-1.
DR WormPep; F4OE10.4; CE32412.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA like lec_gl.
DR InterPro; IPR006207; Cys knot_C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_I1.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF000008; EGF; 7.
DR Pfam; PF02210; Laminin_G_2; 1.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01462; LRRNT; 4.
DR Pfam; PF00560; LRR 1; 17.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00019; LEURICRPT.
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DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_Typ; 7.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 7.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
KW EGF-like domain; Hypothetical protein.
SQ SEQUENCE 1410 AA; 158221 MW; D33716A9C98EBA9D CRC64;

Query Match          54.2%; Score 65; DB 2; Length 1410;
Best Local Similarity 26.9%; Pred. No. 3e+02;
Matches . 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNOXCXQXLDCCSXXCNXXNKCXV 27
DB 938 GFEGDYCEKNIDDCVNSKENGKCV 963

RESULT 40
NTC4_MOUSE
ID NTC4_MOUSE STANDARD; . PRT; 1964 AA.
AC P31695; O35442; O88314; O88316; Q62389; Q62390; Q9R1W9; Q9R1X0;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
GN [Contains: Transforming protein Int-3].
GN Name=Notch4; Synonyms=Int-3, Int3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=92194507; PubMed=1312643;
RA Robbins J., Blondel B.J., Gallahan D., Callahan R.;
RT "Mouse mammary tumor gene int-3: a member of the notch gene family
RT transforms mammary epithelial cells.";
RL J. Virol. 66:2594-2599 (1992).
RN [2];
RP SEQUENCE FROM N.A., AND REVISIONS.
RX MEDLINE=97294599; PubMed=9150355; DOI=10.1038/sj.onc.1201035;
RA Gallahan D., Callahan R.;
RT "The mouse mammary tumor associated gene INT3 is a unique member of
RT the NOTCH gene family (NOTCH4).";
RL Oncogene 14:1883-1890 (1997).
RN [3];
RP SEQUENCE FROM N.A.
RC TISSUE=Lung, and Testis;
RX MEDLINE=96281668; PubMed=8681805;
RA Uyttendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial cell-
RT specific mammalian Notch gene.";
RL Development 122:2251-2259 (1996).
RN [4];
RP SEQUENCE FROM N.A.
RA Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
RA Loretz C., Schmidt S., Traicoff R., Zackrone K., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class III
RT region.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [5];
RP SEQUENCE OF 1436-1600 FROM N.A.
RX MEDLINE=99252212; PubMed=10233982;
RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
RT "Intracisternal type A particle-mediated activation of the Notch4/int3
```

gene in a mouse mammary tumor: generation of truncated Notch4/int3
 mRNAs by retroviral splicing events.";
 J. Virol. 73:5166-5171(1999).
 [6]
 FUNCTION.
 MEDLINE=21244657; PubMed=11344305; DOI=10.1073/pnas.091584598;
 Uytendaele H., Ho J., Rossant J., Kitajewski J.,
 RA "Vascular patterning defects associated with expression of activated
 RT Notch4 in embryonic endothelium";
 Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648 (2001).
 [7]
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
 OF VAL-1463
 RP MEDLINE=21523956; PubMed=11518718; DOI=10.1074/jbc.M107234200;
 Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
 RA "Murine notch homologs (N1-4) undergo presenilin-dependent
 RT proteolysis";
 J. Biol. Chem. 276:40268-40273 (2001).
 [8]
 RP POST-TRANSLATIONAL PROCESSING.
 RP MEDLINE=21374376; PubMed=11459941; DOI=10.1073/pnas.161269998;
 Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RA "Conservation of the biochemical mechanisms of signal transduction
 RT among mammalian Notch family members";
 Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -I- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (By similarity). May regulate branching
 CC morphogenesis in the developing vascular system.
 CC -I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -I- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
 CC kidney, and at lower levels in the ovary and skeletal muscle. A
 CC very low expression is seen in the brain, intestine, liver and
 CC testis.
 CC -I- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
 CC embryonic development from 9.0 dpc.
 CC -I- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane.
 CC -I- PTM: Phosphorylated.
 CC -I- DISEASE: Loss of the extracellular domain causes constitutive
 CC activation of the Notch protein, which leads to hyperproliferation
 CC of glandular epithelial tissues and development of mammary
 CC carcinomas.
 CC -I- SIMILARITY: Belongs to the NOTCH family.
 CC -I- SIMILARITY: Contains 5 ANK repeats.
 CC -I- SIMILARITY: Contains 29 EGF-like domains.
 CC -I- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch.
 CC -----

DR EMBL; M80456; AAB38377.1; -.
 DR EMBL; U43691; AAC52630.1; -.
 DR EMBL; U43691; AAC52631.1; -.
 DR EMBL; AF030001; AAB82004.1; -.
 DR EMBL; AB016771; BAA32281.1; ALT_SEQ.
 DR EMBL; AB016772; BAA32283.1; ALT_INIT.
 DR EMBL; AB016773; BAA32284.1; ALT_INIT.
 DR EMBL; AB016774; BAA32285.1; -.
 DR PIR; A38072; TVMVT3.
 DR PIR; T09059; T09059.
 DR HSSP; P08709; 1BP9.
 DR MGD; MGI:107471; Notch4.
 DR GO; GO:0009886; C:cell surface; ISS.
 DR GO; GO:0005887; C:integral to plasma membrane; ISS.
 DR GO; GO:0005634; C:nucleus; ISS.
 DR GO; GO:0003509; F:calcium ion binding; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0049882; F:protein heterodimerization activity; ISS.
 DR GO; GO:0004872; F:receptor activity; ISS.
 DR GO; GO:0001763; P:branching morphogenesis; IMP.
 DR GO; GO:0030154; P:cell fate determination; ISS.
 DR GO; GO:0001709; P:cell fate determination; ISS.
 DR GO; GO:0009790; P:embryonic development; IMP.
 DR GO; GO:0030097; P:hemoiesis; ISS.
 DR GO; GO:0045602; P:negative regulation of endothelial cell dif. .; IMP.
 DR GO; GO:0007219; P:Notch signaling pathway; TAS.
 DR GO; GO:0001569; P:patterning of blood vessels; IMP.
 DR GO; GO:0045893; P:positive regulation of transcription, DNA-d. .; ISS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; ASX_hydroxyl_S.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 27.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00666; Notch; 2.
 DR PIRSF; PIRSF02279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 11.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS50026; EGF_3; 27.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Activator; ANK repeat; Developmental protein; Differentiation;
 KW Direct protein sequencing; EGF-like domain; Glycoprotein;
 KW Notch signaling pathway; Phosphorylation; Proto-oncogene; Receptor;
 KW Repeat; Signal; transcription regulation; Transmembrane.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 1964 Neurogenic locus notch homolog protein 4.
 FT CHAIN 1411 1964 Transforming protein Int-3.
 FT CHAIN 1428 1964 Notch extracellular truncation.
 FT CHAIN 1463 1964 Notch intracellular domain.
 FT DOMAIN 21 1443 Extracellular (Potential).
 FT TRANSMEM 1444 1464 Potential.
 FT DOMAIN 1465 1964 Cytoplasmic (Potential).
 FT DOMAIN 61 60 EGF-like 1.
 FT DOMAIN 21 112 EGF-like 2.
 FT DOMAIN 115 152 EGF-like 3.
 FT DOMAIN 153 189 EGF-like 4.
 FT DOMAIN 191 229 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN

Db	302	CVCNCGTGCSCQNDICATACVCFHGATC	331
RESULT 43			
NTC3 HUMAN			
ID	NTC3 HUMAN	STANDARD;	PRT; 2321 AA.
AC	Q9UM47; Q9UEB3; Q9UPL3; Q9Y6L8;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-JAN-2005 (Rel. 46, Last annotation update)		
DE	Neurogenic locus notch homolog protein 3 precursor (Notch 3).		
DE	Name=NOTCH3;		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID=9606;		
RN	[1]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=97032728; PubMed=8878478; DOI=10.1038/383707a0;		
RX	Joutel A., Corpechot C., Ducros A., Vahedi K., Chabrier H., Mouton P.,		
RA	Alamowitch S., Domenga V., Cecillon M., Marechal E., Maciazek J.,		
RA	Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,		
RA	Bach J.-F., Bousser M.-G., Tournier-Lasserre E.,		
RT	"Notch3 mutations in CADASIL, a hereditary adult-onset condition		
RT	causing stroke and dementia.";		
RL	Nature 383:707-710(1996).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	Guel M., Artavanis-Tsakonas S.;		
RA	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	PubMed=15057824; DOI=10.1038/nature02399;		
RX	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,		
RA	Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,		
RA	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,		
RA	Caenepeel S., Carrano A.V., Caolle C., Chan Y.M., Christensen M.,		
RA	Cleland A.C., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,		
RA	Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,		
RA	Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,		
RA	Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,		
RA	Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,		
RA	Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,		
RA	Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,		
RA	Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,		
RA	Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,		
RA	Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Uscaszewska A.,		
RA	Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,		
RA	Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,		
RA	Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,		
RA	Rubin E.M., Lucas S.M.;		
RT	"The DNA sequence and biology of human chromosome 19.";		
RL	Nature 428:529-535 (2004).		
RL	[4]		
RN	VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141;		
RP	ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212;		
RP	GLY-222; TYR-242; CYS-258; TYR-542; CYS-558; CYS-578; CYS-728;		
RP	CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS		
RP	ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.		
RX	MEDLINE=98049753; PubMed=9388399; DOI=10.1016/S0140-6736(97)08083-5;		
RA	Joutel A., Vahedi K., Corpechot C., Trosch H., Chabrier H.,		
RA	Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,		
RA	Bach J.-F., Tournier-Lasserre E.;		
RT	"Strong clustering and stereotyped nature of Notch3 mutations in		
RT	CADASIL patients.";		
RL	Lancet 350:1511-1515 (1997).		
RL	[5]		
RN	VARIANT CADASIL 114-GLY--PRO-120 DEL.		
RP	MEDLINE=20264473; PubMed=10802807;		
RA	Joutel A., Chabrier H., Vahedi K., Domenga V., Vayssiere C.,		
RA	Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;		
RT	"Splice site mutation causing a seven amino acid Notch3 in-frame		

Db	302	CVCNCGTGCSCQNDICATACVCFHGATC	331
RESULT 43			
NTC3 HUMAN			
ID	NTC3 HUMAN	STANDARD;	PRT; 2321 AA.
AC	Q9UM47; Q9UEB3; Q9UPL3; Q9Y6L8;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	25-JAN-2005 (Rel. 46, Last annotation update)		
DE	Neurogenic locus notch homolog protein 3 precursor (Notch 3).		
DE	Name=NOTCH3;		
GN	Homo sapiens (Human).		
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OC	NCBI_TaxID:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE:97032728; PubMed=8878478; DOI=10.1038/383707a0;		
RP	Joutel A., Corpechot C., Ducros A., Vahedi K., Chabrier H., Mouton P.,		
RP	Alamowitch S., Domenga V., Cecillon M., Marechal E., Maciazek J.,		
RP	Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,		
RP	Bach J.-F., Bousser M.-G., Tournier-Lasserre E.,		
RP	"Notch3 mutations in CADASIL, a hereditary adult-onset condition		
RP	causing stroke and dementia.";		
RP	Nature 383:707-710(1996).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RP	Guel M., Artavanis-Tsakonas S.;		
RP	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.		
RP	[3]		
RP	SEQUENCE FROM N.A.		
RP	PubMed=15057824; DOI=10.1038/nature02399;		
RP	Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,		
RP	Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,		
RP	Aerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,		
RP	Caenepeel S., Carrano A.V., Caolice C., Chan Y.M., Christensen M.,		
RP	Cleland A.C., Copeland A., Dalin E., Dehal P., Denys M., Deter J.C.,		
RP	Escobar J., Flowers D., Fotopoulos D., Garcia C., Georgescu A.M.,		
RP	Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,		
RP	Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,		
RP	Kobayashi A., Lartionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,		
RP	Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,		
RP	Nelson K., Nolan M., Ovcharenko I., Pitluck S., Pollard J.,		
RP	Popkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,		
RP	Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,		
RP	Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Uscaszewska A.,		
RP	Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,		
RP	Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,		
RP	Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,		
RP	Rubin E.M., Lucas S.M.;		
RP	"The DNA sequence and biology of human chromosome 19.";		
RP	Nature 428:529-535 (2004).		
RP	[4]		
RP	VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141;		
RP	ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212;		
RP	GLY-222; TYR-242; CYS-258; TYR-542; CYS-558; CYS-578; CYS-728;		
RP	CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS		
RP	ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.		
RP	MEDLINE:98049753; PubMed=9388399; DOI=10.1016/S0140-6736(97)08083-5;		
RP	Joutel A., Vahedi K., Corpechot C., Trosch H., Chabrier H.,		
RP	Vayssiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,		
RP	Bach J.-F., Tournier-Lasserre E.;		
RP	"Strong clustering and stereotyped nature of Notch3 mutations in		
RP	CADASIL patients.";		
RP	Lancet 350:1511-1515 (1997).		
RP	[5]		
RP	VARIANT CADASIL 114-GLY--PRO-120 DEL.		
RP	MEDLINE-20264473; PubMed=10802807;		
RP	Joutel A., Chabrier H., Vahedi K., Domenga V., Vayssiere C.,		
RP	Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.;		
RP	"Splice site mutation causing a seven amino acid Notch3 in-frame		

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DR EMBL; AF058899; AAC14346.1; JOINED.
DR EMBL; AC004257; AAC04897.1; -.
DR EMBL; AC004663; AAC15789.1; ALT_INIT.
DR PIR; S78549; S78549.
DR HSSP; P00740; IEDM.
DR Genew; HGNC:7883; NOTCH3.
DR MIM; 600276; -.
DR MIM; 125310; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR008985; ConA-like lec_gl.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR010660; NOD-like.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF00008; EGF; 34.
DR Pfam; PF06816; NOD; 1.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF02279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF CA; 19.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50297; ANK REP REGION; 1.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 18.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS50026; EGF_3; 34.
DR PROSITE; PS01187; EGF CA; 16.
KW Activator; ANK repeat; Developmental protein; Differentiation;
KW Disease mutation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Phosphorylation; Polymorphism; Receptor;
KW Repeat; Signal; Transcription regulation; Transmembrane.
FT SIGNAL 1 39 Potential.
FT CHAIN 40 2321 Notch extracellular truncation (By
FT CHAIN 1629 2321 similarity).
FT CHAIN 1662 2321 Notch intracellular domain (By
FT CHAIN 40 1643 similarity).
FT DOMAIN 1644 1664 Extracellular (Potential).
FT TRANSMEM 1665 2321 Potential.
FT DOMAIN 40 77 Cytoplasmic (Potential).
FT DOMAIN 78 118 EGF-like 1.
FT DOMAIN 119 156 EGF-like 2.
FT DOMAIN 158 195 EGF-like 3.
FT DOMAIN 197 234 EGF-like 5.
FT DOMAIN 236 272 EGF-like 6.
FT DOMAIN 312 350 EGF-like 7.
FT DOMAIN 374 429 EGF-like 8.
FT DOMAIN 351 389 EGF-like 9.
FT DOMAIN 391 429 EGF-like 10, calcium-binding (Potential).
FT DOMAIN 431 467 EGF-like 11, calcium-binding (Potential).

Query Match 54.2%; Score 65; DB 1; Length 2321;
Best Local Similarity 30.0%; Pred. No. 4.7e+02;
Matches 9; Conservative 13; Mismatches 4; Indels 4; Gaps 1;

QY 1 CXIXN---QXCXQLDDCCSXCNXNXC 26
| : : : : : : : : : : : : : : : : : :
Db 300 CVCVNGWTGSCSQNIDCATVCFHGATC 329

RESULT 44
O16004 PRELIMINARY; PRT; 2531 AA.
ID O16004

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AC O16004;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT PIR; S78549; S78549.
DT HSSP; P00740; IEDM.
DE Notch homolog.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454256; PubMed=9310331;
RA Sherwood D.R., McClay D.R.;
RT "Identification and localization of a sea urchin Notch homologue:
RT insights into vegetal plate regionalization and Notch receptor
RT regulation.";
RL Development 124:3363-3374(1997).
DR EMBL; AF000634; AAB82088.1; -.
DR PIR; T31070; T31070.
DR HSSP; P01132; IEGF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR GO; GO:0050793; P:regulation of development; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_region.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF00008; EGF; 31.
DR Pfam; PF07645; EGF CA; 4.
DR Pfam; PF00066; Notch; 3.
DR PIRSF; PIRSF02279; Notch; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF CA; 23.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 21.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS50026; EGF_3; 35.
DR PROSITE; PS01187; EGF CA; 20..
KW ANK repeat; EGF-like domain.
SQ SEQUENCE 2531 AA; 5BF42BEC627CA303 CRC64;

Query Match 54.2%; Score 65; DB 2; Length 2531;
Best Local Similarity 38.1%; Pred. No. 5.1e+02;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

QY 7 XCXQLDDCCSXCNXNXC 27
| : : : : : : : : : : : : : : : :
Db 661 NCEEDIDDCSRPCHNGGTCV 681

RESULT 45
Q25253
ID O25253 PRELIMINARY; PRT; 2653 AA.
AC Q25253;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch homolog Scalloped wings.
GN Name=Sc;
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).

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	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC	Calliphoridae; Lucilia.
OX	NCBI_TaxID=7375;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SS seeking;
RX	MEDLINE=96400928; PubMed=8807304;
RA	Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L., McKenzie J.A., Batterham P.;
RA	"Scalloped wings is the Lucilia cuprina Notch homologue and a candidate for the modifier of fitness and asymmetry of diazinon resistance.";
RT	Genetics 143:1321-1337(1996).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	STRAIN=SS seeking;
RC	MEDLINE=98426367; PubMed=9753770; DOI=10.1016/S0965-1748(98)00032-0;
RX	Chen Z., Newsome T., McKenzie J.A., Batterham P.;
RA	"Molecular characterization of the Notch homologue from the Australian sheep blowfly, Lucilia cuprina";
RT	Insect Biochem. Mol. Biol. 28:601-612(1998).
RL	ENBL; U58977; AAC36151.1;
DR	HSP; P07207; IOT8.
DR	GO; GO:001620; C:membrane; IEA.
DR	GO; GO:000509; F:calcium ion binding; IEA.
DR	GO; GO:0030154; P:cell differentiation; IEA.
DR	GO; GO:0050793; P:regulation of development; IEA.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR000152; Asx_hydroxyl_S.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR001438; EGF-II.
DR	InterPro; IPR006209; EGF-like.
DR	InterPro; IPR008297; Notch.
DR	InterPro; IPR000800; Notch_region.
DR	Pfam; PF00023; Ank; 6.
DR	Pfam; PF00008; EGF; 31.
DR	Pfam; PF07645; EGF_CA; 3.
DR	Pfam; PF00066; NotCh; 3.
DR	PIRSF; PIRSF002279; Notch; 1.
DR	PRINTS; PR01415; ANKYRN.
DR	PRINTS; PRO0010; EGFBLOOD.
DR	PRINTS; PR01452; NOTCH.
DR	SMART; SM00248; ANK; 7.
DR	SMART; SM00179; EGF_CA; 24.
DR	SMART; SM00004; NL_3.
DR	PROSITE; PS50088; ANK_REPEAT; 5.
DR	PROSITE; PS50297; ANK_REP_REGION; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 22.
DR	PROSITE; PS00022; EGF_1; 34.
DR	PROSITE; PS01186; EGF_2; 28.
DR	PROSITE; PS50026; EGF_3; 36.
DR	PROSITE; PS01187; EGF_CA; 21.
KW	ANK repeat; EGF-like domain.
SQ	SEQUENCE 2653 AA; 285928 MW; 6AF2A058FEFC6329 CRC64;
	Query Match 54.2%; Score 65; DB 2; Length 2653;
	Best Local Similarity 29.2%; Pred.No. 5.3e+02;
	Matches 7; Conservative 12; Mismatches 5; Indels 0; Gaps
Qy	4 XNQXCXXQLDDCCSXCNXKNXCV 27 : :: :: :: :
Db	268 QGNCEQNIDDGPHLCQGNGTCI 291 : :: :: :: :
RESULT 46	
Q646V4	PRELIMINARY; PRT; 74 AA.
ID	Q646V4
AC	Q646V4;
DT	25-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)


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RX MEDLINE=98148073; PubMed=9478979; DOI=10.1074/jbc.273.9.5235;
RA Moestrup S.K., Kozyraki R., Kristiansen M., Kayen J.H.,
RA Rasmussen H.H., Brault D., Pontillon F., Goda F.O., Christensen E.I.,
RA Hammond T.G., Verroust P.J.;
RT "The intrinsic factor-vitamin B12 receptor and target of teratogenic
RT antibodies is a megalin-binding peripheral membrane protein with
RT homology to developmental proteins.";
RL J. Biol. Chem. 273:5235-5242(1998).
DR EMBL; AF022247; AAC71661.1;
DR PIR; T08618; T08618.
DR HSP; P00740; 11XA.
DR GO; GO:000509; F:calcium ion binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000742; EGF_Ca.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00431; CUB; 27.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF07645; EGF_Ca; 3.
DR SMART; SM00042; CUB; 27.
DR SMART; SM00179; EGF_Ca; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01180; CUB; 27.
DR PROSITE; PS00022; EGF_1; 4.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 4.
KW EGF-like domain; Receptor; Signal.
FT SIGNAL 1 20
FT CHAIN 21 3623
FT INTRINSIC factor-B12 receptor.
SQ SEQUENCE 3623 AA; 398984 MW; 39FB792AC6545240 CRC64;

Query Match 53.3%; Score 64; DB 2; Length 3623;
Best Local Similarity 29.2%; Pred. No. 8.9e+02;
Matches 7; Conservative 13; Mismatches 4; Indels 0; Gaps 0;

OY 4 XNOXCXQXLDCCSXCNXNKCXV 27
DB 425 SQQNCNTENINDSSNPLNGGTGCI 448

RESULT 55
MTB COLVI STANDARD; PRT; 43 AA.
AC P27087;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Metallothionein B (MTB) (Fragment).
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Odontophoridae; Colinus.
OX NCBI_TaxID=9014;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93247066; PubMed=8493164;
RA Shartzer K.L., Kage K., Sobleski R.J., Andrews G.K.;
RT "Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail.";
RL J. Mol. Evol. 36:255-262(1993).
CC -!- FUNCTION: Metallothioneins have a high content of cysteine
CC residues that bind various heavy metals.
CC -!- DOMAIN: Class I metallothioneins contain 2 metal-binding domains:
CC four divalent ions are chelated within cluster A of the alpha
CC domain and are coordinated via cysteinyl thiolate bridges to 11
CC cysteine ligands. Cluster B, the corresponding region within the
CC beta domain, can ligate three divalent ions to 9 cysteines.
CC -!- SIMILARITY: Belongs to the metallothionein superfamily. Family 1.

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CC -----
DR EMBL; X62512; CAA44371.1;
DR PIR; S33379; S18174.
DR HSP; P04355; 1MRT.
DR InterPro; IPR003019; Metallthion.
DR InterPro; IPR000006; Metallthion_1.
DR InterPro; IPR001212; Somatomedin_B.
DR Pfam; PF00131; Metallothio; 1.
DR PRINTS; PR00860; MTVERTERATE.
DR PRINTS; PR00022; SOMATOMEDINE.
DR PROSITE; PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster.
FT NON_TER 1 1
FT DOMAIN <1 16 Beta.
FT DOMAIN 17 >43 Alpha.
FT METAL 2 2 Cluster B.
FT METAL 6 6 Cluster B.
FT METAL 8 8 Cluster B.
FT METAL 11 11 Cluster B.
FT METAL 13 13 Cluster B.
FT METAL 16 16 Cluster B.
FT METAL 20 20 Cluster A.
FT METAL 21 21 Cluster A.
FT METAL 23 23 Cluster A.
FT METAL 24 24 Cluster A.
FT METAL 28 28 Cluster A.
FT METAL 31 31 Cluster A.
FT METAL 35 35 Cluster A.
FT METAL 37 37 Cluster A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA; 4429 MW; 1612EB40E6EB875 CRC64;

Query Match 52.5%; Score 63; DB 1; Length 43;
Best Local Similarity 33.3%; Pred. No. 20;
Matches 9; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

OY 1 CXIXNQXCQXLDCCSXCNXNKCXV 27
DB 6 CKCKNCRCSCKSCSCCPCAGCNVCV 32

RESULT 56
FBP3_STRPU STANDARD; PRT; 570 AA.
AC P49013;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibropellin_C precursor (Epidermal growth factor-related protein 3)
DE (EGF III) (Fibropellin III).
GN Name=EGF3;
OS Strongylocentrotus purpuratus (Purple sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoida; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
OC Strongylocentrotus.
OX NCBI_TaxID=7668;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula;
RX MEDLINE=93273088; PubMed=8500658; DOI=10.1006/dbio.1993.1155;
RA Bisgrove B.W., Raff R.A.;
RT "The SpSGF III gene encodes a member of the fibropellins: EGF repeat-
RT containing proteins that form the apical lamina of the sea urchin
RT embryo.";
RL Dev. Biol. 157:526-538(1993).
CC -!- FUNCTION: Forms the apical lamina, a component of the

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DT	InterPro; IPR006210; IEGF.
DR	InterPro; IPR001005; Myb_DNA_binding.
DR	Pfam; PF00008; EGF_5.
DR	PRINTS; PR00010; EGFBLOOD.
DR	SMART; SM00181; EGF; 6.
DR	PROSITE; PS00022; EGF_1; 6.
DR	PROSITE; PS01186; EGF_2; 6.
DR	PROSITE; PS50026; EGF_3; 5.
DR	PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW	EGF-like domain.
SQ	SEQUENCE 585 AA; 61125 MW; EB276F08998D4E9 CRC64;
Query Match	52.5%; Score 63; DB 2; Length 585;
Best Local Similarity	30.8%; Pred. No. 2.1e+02;
Matches	8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
OY	2 XIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db	380 GFAGPRCEHLDLDCAGRACANGGTCV 405
RESULT 58	
QNBS4	
ID	QNBS4 PRELIMINARY; PRT; 587 AA.
AC	QNBS4;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein FLJ90821.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA	Suzuki Y., Nagai K., Sugano S., Isnii S., Kawai-Hio Y., Saito K.,
RA	Yanamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA	Maehno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
RL	Submitted (MAR-2002) to the EMBL/GenBank/DDAJ databases.
CC	-!- SIMILARITY: Contains 6 EGF-like domains.
CC	EMBL; AK075302; BAC11535.1; -.
DR	HSP; P00740; IEDM.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR001438; EGF_I.
DR	InterPro; IPR006209; EGF_like.
DR	Pfam; PF00008; EGF; 5.
DR	PRINTS; PR00010; EGFBLOOD.
DR	PROSITE; PS00022; EGF_1; 6.
DR	PROSITE; PS01186; EGF_2; 6.
DR	PROSITE; PS50026; EGF_3; 5.
DR	Pfam; PF00008; EGF; 5.
DR	PRINTS; PR00010; EGFBLOOD.
DR	SMART; SM00181; EGF; 6.
DR	PROSITE; PS00022; EGF_1; 6.
DR	PROSITE; PS01186; EGF_2; 6.
DR	PROSITE; PS50026; EGF_3; 5.
DR	PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW	EGF-like domain.
SQ	SEQUENCE 587 AA; 61144 MW; 2PF5E3EA66789B1B CRC64;
Query Match	52.5%; Score 63; DB 2; Length 587;
Best Local Similarity	30.8%; Pred. No. 2.1e+02;
Matches	8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
OY	2 XIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db	382 GFAGPRCEHLDLDCAGRACANGGTCV 407
RESULT 59:	
DLL3_RAT	
ID	DLL3_RAT STANDARD; PRT; 569 AA.
AC	O88671;
DT	16-OCT-2001 (Rel. 40, Created)

DT	InterPro; IPR006210; IEGF.
DR	InterPro; IPR001005; Myb_DNA_binding.
DR	Pfam; PF00008; EGF_5.
DR	PRINTS; PR00010; EGFBLOOD.
DR	SMART; SM00181; EGF; 6.
DR	PROSITE; PS00022; EGF_1; 6.
DR	PROSITE; PS01186; EGF_2; 6.
DR	PROSITE; PS50026; EGF_3; 5.
DR	PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW	EGF-like domain.
SQ	SEQUENCE 585 AA; 61125 MW; EB276F08998D4E9 CRC64;
Query Match	52.5%; Score 63; DB 2; Length 585;
Best Local Similarity	30.8%; Pred. No. 2.1e+02;
Matches	8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
OY	2 XIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db	380 GFAGPRCEHLDLDCAGRACANGGTCV 405
RESULT 58	
QNBS4	
ID	QNBS4 PRELIMINARY; PRT; 587 AA.
AC	QNBS4;
DT	01-OCT-2002 (TrEMBLrel. 22, Created)
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Hypothetical protein FLJ90821.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Isoqai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA	Suzuki Y., Nagai K., Sugano S., Isnii S., Kawai-Hio Y., Saito K.,
RA	Yanamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA	Maehno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.,
RL	Submitted (MAR-2002) to the EMBL/GenBank/DDAJ databases.
CC	-!- SIMILARITY: Contains 6 EGF-like domains.
CC	EMBL; AK075302; BAC11535.1; -.
DR	HSP; P00740; IEDM.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR001438; EGF_II.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR006210; IEGB.
DR	Pfam; PF00008; EGF; 5.
DR	PRINTS; PR00010; EGFBLOOD.
DR	SMART; SM00181; EGF; 6.
DR	PROSITE; PS00022; EGF_1; 6.
DR	PROSITE; PS01186; EGF_2; 6.
DR	PROSITE; PS50026; EGF_3; 6.
DR	PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW	EGF-like domain.
SQ	SEQUENCE 587 AA; 61144 MW; 2PF5E3EA66789B1B CRC64;
Query Match	52.5%; Score 63; DB 2; Length 587;
Best Local Similarity	30.8%; Pred. No. 2.1e+02;
Matches	8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
OY	2 XIXNQXCXQLDDCCSXCNXXNKCVCV 27
Db	382 GFAGPRCEHLDLDCAGRACANGGTCV 407
RESULT 59:	
DLL3_RAT	
ID	DLL3_RAT STANDARD; PRT; 569 AA.
AC	O88671;
DT	16-OCT-2001 (Rel. 40, Created)

L -> P (in dbSNP:1110627).

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FT VARIANT 385 385 /FTID=VAR_016776.
FT FT G-> D (in SCD01).
FT FT /FTID=VAR_009952.
SQ SEQUENCE 618 AA; 64617 MW; 58A9BC0A7DEAD1A0 CRC64;

Query Match 52.5%; Score 63; DB 1; Length 618;
Best Local Similarity 30.8%; Pred. No. 2.2e+02;
Matches 8; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXXCNXKCV 27
Db 382 GFAGPRCEHLDLDDCAGRACANGGTCV 407

RESULT 62
ID P79941 PRELIMINARY; PRT; 642 AA.
AC P79941;
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE Notch ligand X-Delta-2.
GN Name=X-Delta-2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Jen W.C., Wettstein D.A., Chitnis A.B., Kintner C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U70843; AAB37131.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005509; F.calcium ion binding; IEA.
DR GO; GO:0007154; P.cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_Ca; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 2.
DR EGF-like domain.
SQ SEQUENCE 642 AA; 70667 MW; D7DC31EB9D92820C CRC64;

Query Match 52.5%; Score 63; DB 2; Length 642;
Best Local Similarity 30.8%; Pred. No. 2.3e+02;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 2 XIXNQXCQXLDCCSXXCNXKCV 27
Db 415 GFSGPRCELNDDCASSPCANGGTCV 440

RESULT 63
Q7ZXT4
ID Q7ZXT4 PRELIMINARY; PRT; 642 AA.
AC Q7ZXT4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 26, Last annotation update)

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DE MCS2561 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044262; AAH44262.1; -.
DR HSSP; P00740; 1EDM.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005509; F.calcium ion binding; IEA.
DR GO; GO:0007154; P.cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF07645; EGF_Ca; 1.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_Ca; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS01187; EGF_Ca; 2.
DR EGF-like domain.
SQ SEQUENCE 642 AA; 70655 MW; 56AFB4013E1C2AE2 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 642;
Best Local Similarity 30.8%; Pred. No. 2.3e+02;
Matches 8; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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QY      2 XIXNOXCXOXLDCCSXCNXXNCV 27
Db      415 GFSGPCELNIDCASPANGTCV 440

RESULT 64
JAG2_RAT
ID      JAG2_RAT      STANDARD;      PRT; 1202 AA.
AC      P97607;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      Jagged2 (Jagged2) (Fragment).
GN      Name=Jag2;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN      NCBI_TaxID=10116;
RP      [1]
RC      SEQUENCE FROM N.A.
RX      TISSUE=Brain;
RA      MEDLINE=97105852; PubMed=8948600; DOI=10.1006/dbio.1996.0310;
RT      Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
RL      "Jagged2: a serrate-like gene expressed during rat embryogenesis.";
CC      Dev. Biol. 180:370-376(1996).
CC      -!- FUNCTION: Putative Notch ligand involved in the mediation of Notch
CC      signaling. May have a role in neurogenesis in the peripheral
CC      nervous system, limb development and in the adult brain.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- DEVELOPMENTAL STAGE: At stage E12.5 it is detected in dorsal root
CC      ganglia, AER, and surface ectoderm. At E14.5, found as well in
CC      cranial ganglia, thymus and olfactory epithelia. At E16.5, found as
CC      well in salivary gland, tooth buds and hair follicles.
CC      -!- SIMILARITY: Contains 1 DSL domain.
CC      -!- SIMILARITY: Contains 16 EGF-like domains.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U70050; AAC52946.1; -.
DR      HSP; P00743; ICCF.
DR      RGD; 2938; Jag2.
DR      GO; GO:0005887; C: integral to plasma membrane; ISS.
DR      GO; GO:0008083; F: growth factor activity; ISS.
DR      GO; GO:0005112; F: Notch binding; NAS.
DR      GO; GO:0007049; P: cell cycle; ISS.
DR      GO; GO:0030154; P: cell differentiation; NAS.
DR      GO; GO:0001709; P: cell fate determination; NAS.
DR      GO; GO:0009912; P: hair cell fate commitment; ISS.
DR      GO; GO:0030326; P: limb morphogenesis; NAS.
DR      GO; GO:0007219; P: Notch signaling pathway; NAS.
DR      GO; GO:0007605; P: perception of sound; ISS.
DR      GO; GO:0030334; P: regulation of cell migration; ISS.
DR      GO; GO:0042127; P: regulation of cell proliferation; ISS.
DR      GO; GO:0007283; P: spermatogenesis; IEP.
DR      GO; GO:0030217; P: T-cell differentiation; ISS.
DR      GO; GO:0045061; P: thymic T-cell selection; ISS.
DR      InterPro; IPR000152; Asx_hydroxyl_S.
DR      InterPro; IPR001774; DSL.
DR      InterPro; IPR000742; EGF_2.
DR      InterPro; IPR001881; EGF_Ca.
DR      InterPro; IPR001438; EGF_II.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR009041; PMP_SGCI.
DR      Pfam; PF01414; DSL_1.
DR      Pfam; PF00008; EGF_14.
DR      PRINTS; PR00010; EGFBLD.
DR      PROSITE; PS00010; ASX_HYDROXYL; 10.

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DR      PROSITE; PS00022; EGF_1; 15.
DR      PROSITE; PS01186; EGF_2; 11.
DR      PROSITE; PS00026; EGF_3; 15.
DR      PROSITE; PS01187; EGF_CA; 7.
KW      Calcium-binding; Developmental protein; EGF-like domain; Glycoprotein;
KW      Notch signaling pathway; Repeat; Transmembrane.
FT      NON_TER 1
FT      DOMAIN <1 1085 Extracellular (Potential).
FT      TRANSMEM 1086 1102 Potential.
FT      DOMAIN 1103 1202 Cytoplasmic (Potential).
FT      DSL-like 1 132 194 DSL-like 1.
FT      EGF-like 2 195 228 EGF-like 2.
FT      EGF-like 3 229 259 EGF-like 3.
FT      EGF-like 4 261 299 EGF-like 4.
FT      EGF-like 5 301 337 EGF-like 5, calcium-binding (Potential).
FT      EGF-like 6 339 375 EGF-like 6, calcium-binding (Potential).
FT      EGF-like 7 377 413 EGF-like 7, calcium-binding (Potential).
FT      EGF-like 8 415 450 EGF-like 8.
FT      EGF-like 9 452 488 EGF-like 9.
FT      EGF-like 10 490 527 EGF-like 10 (atypical).
FT      EGF-like 11 529 589 EGF-like 11, calcium-binding (Potential).
FT      EGF-like 12 591 627 EGF-like 12, calcium-binding (Potential).
FT      EGF-like 13 629 665 EGF-like 13.
FT      EGF-like 14 667 703 EGF-like 14.
FT      EGF-like 15 706 742 EGF-like 15, calcium-binding (Potential).
FT      EGF-like 16 744 780 EGF-like 16, calcium-binding (Potential).
FT      DISULFID 782 818 By similarity.
FT      DISULFID 199 210 By similarity.
FT      DISULFID 203 216 By similarity.
FT      DISULFID 218 227 By similarity.
FT      DISULFID 230 241 By similarity.
FT      DISULFID 246 258 By similarity.
FT      DISULFID 259 277 By similarity.
FT      DISULFID 271 287 By similarity.
FT      DISULFID 289 298 By similarity.
FT      DISULFID 305 316 By similarity.
FT      DISULFID 310 325 By similarity.
FT      DISULFID 327 336 By similarity.
FT      DISULFID 343 354 By similarity.
FT      DISULFID 368 374 By similarity.
FT      DISULFID 381 392 By similarity.
FT      DISULFID 386 401 By similarity.
FT      DISULFID 403 412 By similarity.
FT      DISULFID 419 429 By similarity.
FT      DISULFID 423 438 By similarity.
FT      DISULFID 440 449 By similarity.
FT      DISULFID 456 467 By similarity.
FT      DISULFID 461 476 By similarity.
FT      DISULFID 478 487 By similarity.
FT      DISULFID 495 506 By similarity.
FT      DISULFID 500 515 By similarity.
FT      DISULFID 517 526 By similarity.
FT      DISULFID 544 567 Potential.
FT      DISULFID 561 577 Potential.
FT      DISULFID 579 588 By similarity.
FT      DISULFID 595 606 By similarity.
FT      DISULFID 600 615 By similarity.
FT      DISULFID 617 626 By similarity.
FT      DISULFID 633 644 By similarity.
FT      DISULFID 638 653 By similarity.
FT      DISULFID 655 664 By similarity.
FT      DISULFID 671 682 By similarity.
FT      DISULFID 676 691 By similarity.
FT      DISULFID 693 702 By similarity.
FT      DISULFID 710 721 By similarity.
FT      DISULFID 715 730 By similarity.
FT      DISULFID 732 741 By similarity.
FT      DISULFID 748 759 By similarity.
FT      DISULFID 753 768 By similarity.
FT      DISULFID 770 779 By similarity.
FT      DISULFID 786 797 By similarity.

```


FT	DOMAIN	636	672	EGF-like 11, calcium-binding (Potential).
FT	DOMAIN	674	710	EGF-like 12, calcium-binding (Potential).
FT	DOMAIN	712	748	EGF-like 13.
FT	DOMAIN	751	787	EGF-like 14.
FT	DOMAIN	789	825	EGF-like 15, calcium-binding (Potential).
FT	DOMAIN	827	863	EGF-like 16, calcium-binding (Potential).
FT	DOMAIN	870	944	WFCC.
FT	DISULFID	245	256	By similarity.
FT	DISULFID	249	262	By similarity.
FT	DISULFID	264	273	By similarity.
FT	DISULFID	276	287	By similarity.
FT	DISULFID	282	293	By similarity.
FT	DISULFID	295	304	By similarity.
FT	DISULFID	311	323	By similarity.
FT	DISULFID	317	333	By similarity.
FT	DISULFID	335	344	By similarity.
FT	DISULFID	351	362	By similarity.
FT	DISULFID	356	371	By similarity.
FT	DISULFID	373	382	By similarity.
FT	DISULFID	389	400	By similarity.
FT	DISULFID	394	409	By similarity.
FT	DISULFID	411	420	By similarity.
FT	DISULFID	427	438	By similarity.
FT	DISULFID	432	447	By similarity.
FT	DISULFID	449	458	By similarity.
FT	DISULFID	465	475	By similarity.
FT	DISULFID	469	484	By similarity.
FT	DISULFID	486	495	By similarity.
FT	DISULFID	502	513	By similarity.
FT	DISULFID	507	522	By similarity.
FT	DISULFID	524	533	By similarity.
FT	DISULFID	540	551	By similarity.
FT	DISULFID	545	560	By similarity.
FT	DISULFID	562	571	By similarity.
FT	DISULFID	589	612	Potential.
FT	DISULFID	606	622	Potential.
FT	DISULFID	624	633	By similarity.
FT	DISULFID	640	651	By similarity.
FT	DISULFID	645	660	By similarity.
FT	DISULFID	662	671	By similarity.
FT	DISULFID	678	689	By similarity.
FT	DISULFID	683	698	By similarity.
FT	DISULFID	700	709	By similarity.
FT	DISULFID	716	727	By similarity.
FT	DISULFID	721	736	By similarity.
FT	DISULFID	738	747	By similarity.
FT	DISULFID	755	766	By similarity.
FT	DISULFID	760	775	By similarity.
FT	DISULFID	777	786	By similarity.
FT	DISULFID	793	804	By similarity.
FT	DISULFID	798	813	N-linked (GlcNAc...) (Potential).
FT	DISULFID	815	824	N-linked (GlcNAc...) (Potential).
FT	DISULFID	831	842	N-linked (GlcNAc...) (Potential).
FT	DISULFID	836	851	N-linked (GlcNAc...) (Potential).
FT	DISULFID	853	862	N-linked (GlcNAc...) (Potential).
FT	CARBOHYD	133	153	Missing (in isoform Short).
FT	CARBOHYD	570	570	FT/Id-VSP 001395
FT	CARBOHYD	619	619	RLPRR -> AFPPA (in Ref. 1).
FT	CARBOHYD	752	752	A -> P (in Ref. 1).
FT	CARBOHYD	1058	1058	L -> F (in Ref. 1).
FT	VARSPPLIC	424	461	L -> SA (in Ref. 4).
FT	CONFLICT	8	12	ANE -> VND (in Ref. 1).
FT	CONFLICT	119	119	K -> E (in Ref. 3; AAD15562 and 4).
FT	CONFLICT	128	129	A -> V (in Ref. 2).
FT	CONFLICT	384	384	
FT	CONFLICT	424	426	
FT	CONFLICT	501	501	
FT	CONFLICT	1235	1235	

Query Match

Query Match 52.5%; Score 63; DB 1; Length 1238;

Best Local Similarity

```

QY      2 XIXNQXCKXKLDCCSXCNXXNXCVCV 27
DB      : : : : : : : : : : : : : : : :
        627 GFTGTYCHENIDDLGLGPCRNGGTCTCI 652

RESULT 66
JAG2 MOUSE
ID   JAG2_MOUSE          STANDARD;             PRT;    1247 AA.
AC   Q9OYES; O55139; O70219;
DT   28-FEB-2003 (Rel. 41, Created)
DD   28-FEB-2003 (Rel. 41, Last sequence update)
DE   25-JAN-2005 (Rel. 46, Last annotation update)
GN   Jagged 2 precursor (Jagged2).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
NCBI_TaxID=10090;
RP   SEQUENCE FROM N.A.
RA   STRAIN=Swiss Webster / NIH;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DBJP databases.
[2]
RP   SEQUENCE OF 325-819 FROM N.A.
RC   TISSUE=Brain;
RD   MEDLINE=98051918; PubMed=9341252;
RE   Lan Y., Jiang R., Shawber C., Weinmaster G., Gridley T.;
RF   "The Jagged2 gene maps to chromosome 12 and is a candidate for the Lgl
RG   and sm mutations.";
RH   Mamm. Genome 8:875-876(1997).
RI   [3]
RP   SEQUENCE OF 325-759 FROM N.A.
RC   TISSUE=Brain;
RD   MEDLINE=98145947; PubMed=9486542; DOI=10.1016/S0925-4773(97)00146-9;
RE   Valecchi C., Ghezzi C., Ballabio A., Rugari E.L.;
RF   "Jagged2: a putative Notch ligand expressed in the apical ectodermal
RG   ridge and in sites of epithelial-mesenchymal interactions.";
RH   Mech. Dev. 69:203-207(1997).
RI   [4]
RP   TISSUE SPECIFICITY.
RD   MEDLINE=97459705; PubMed=9315665;
RE   Luo B., Aster J.C., Hasseljian R.P., Kuo F., Sklar J.;
RF   "Isolation and functional analysis of a cDNA for human Jagged2, a gene
RG   encoding a ligand for the Notchl receptor.";
RH   Mol. Cell. Biol. 17:6057-6067(1997).
RI   [-] FUNCTION: Putative Notch ligand involved in the mediation of Notch
RG   signaling. Plays an essential role during limb, craniofacial and
RD   thymic development. May be involved in myogenesis and in the
RE   development of peripheral and central nervous systems.
RF   [-] SUBCELLULAR LOCATION: Type I membrane protein.
RG   [-] TISSUE SPECIFICITY: Found to be highest in fetal thymus,
RD   epidermis, foregut dorsal root ganglia and inner ear. In 2-week-
RE   old mice, abundant in heart, lung, thymus, skeletal muscle, brain
RF   and testis. Expression overlaps partially with Notchl expression.
RG   [-] DEVELOPMENTAL STAGE: At 13 dpc, found in paravertebral vessels and
RD   dorsal root ganglia. At 14 dpc, in oropharyngeal epithelium,
RE   developing thymus and in the muscles of the tongue. By 15 dpc, in
RF   many tissues.
RG   [-] SIMILARITY: Contains 1 DSL domain.
RD   [-] SIMILARITY: Contains 16 EGF-like domains.
CC   -----
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announ
CC   or send an email to licens@isb-sib.ch).
CC   -----
EMBL; AF038572; AACF16411.1; --
DR   EMBL; AF010137; AACI4010.1; --

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RC STRAIN=C57BL/6J; TISSUE=Whole embryo;
RX MEDLINE=98142023; PubMed=9473344; DOI=10.1006/excr.1997.3865;
RA Hoff H.B. III, Tresini M., Li S., Sell C.;
RT "DBI-1, a novel gene related to the notch family, modulates mitogenic
RL response to insulin-like growth factor 1.";
RR EMBL; U57368; AAB01338.1; -.
DR PIR; T30176; T30176.
DR HSP; P08709; 1F7E.
DR MGD; MGI:1202397; Ddx26.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000629; DEAD box.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR009030; Grow_fac_recept.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF07645; EGF_Ca; 1.
DR SMART; SM00179; EGF_CA; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00039; DEAD ATP HELICASE; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_Ca; 2.
DR EGF-like domain; Transmembrane.
SQ SEQUENCE 1687 AA; 188528 MW; DA3B5302B67545D3 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 1687;
Best Local Similarity 26.9%; Pred. No. 5.6e+02;
Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXQXQXLDCCSXXCNXNKCXV 27
Db 480 GFEGSTCERNIDCPNHNKONGVCV 505

RESULT 68
Q7QCP4
ID Q7QCP4 PRELIMINARY; PRT; 3523 AA.
AC Q7QCP4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AgCP1653 (Fragment).
GN Name=agCG50053; ORFNames=ENSANGG00000007782;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAB0100859; EAA08121.1; -.
DR HSP; P00740; 1EDM.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR000895; ConA_like_lec_gl.
DR InterPro; IPR000859; CUB_like_1.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
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DR InterPro; IPR000421; FA58_C.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR003410; Hyalin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 3.
DR Pfam; PF00008; EGF; 11.
DR Pfam; PF07645; EGF_Ca; 2.
DR Pfam; PF02494; HVR; 3.
DR Pfam; PF00057; Ldl_recept_a; 1.
DR Pfam; PF00059; Lectin_C; 1.
DR Pfam; PF00084; Sushi; 8.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX HYDROXYL; 11.
DR PROSITE; PS01180; CUB; 3.
DR PROSITE; PS00041; C TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF_1; 15.
DR PROSITE; PS01186; EGF_2; 13.
DR PROSITE; PS00026; EGF_3; 17.
DR PROSITE; PS01187; EGF_Ca; 7.
DR PROSITE; PS00022; FA58C_3; 2.
DR PROSITE; PS00825; HVR; 3.
DR PROSITE; PS01209; LDLRA_1; 1.
DR PROSITE; PS00068; LDLRA_2; 1.
DR PROSITE; PS00923; SUSHI; 6.
KW EGF-like domain.
FT NON TER 1
FT NON TER 3523
SQ SEQUENCE 3523 AA; 385001 MW; B58BB58E2A484E6 CRC64;

Query Match 52.5%; Score 63; DB 2; Length 3523;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 8; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

Qy 4 XNQXQXQXLDCCSXXCNXNKCXV 27
Db 2247 TKNQCHTVDDCESAPQNGGTCV 2270

RESULT 69
CX07_CONGE
ID CX07 CONGE STANDARD; PRT; 29 AA.
AC P05483;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxins GVIIA/GVIIB (Shaker peptides GVIIA/GVIIB) (SNX-178).
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=86070213; PubMed=4071055;
RA Oliveira B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
RA Rivier J.E., de Santos V., Cruz L.J.;
RT "Peptide neurotoxins from fish-hunting cone snails.";
RL Sequence 230:1338-1343(1985).
CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MISCELLANEOUS: The sequence shown is that of conotoxin GVIIA.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
DR PIR; A43620; A43620.
DR PIR; B43620; B43620.
KW Calcium channel inhibitor; Direct protein sequencing; Hydroxylation;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
MOD_RES 4 4 4-hydroxyproline.
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CC similarity). This toxin blocks N-type calcium channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
CC
DR HSSP; P05484; 1DM4.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
DR Amindat; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
KW Toinin.
KW FT SIGNAL 1 22 Potential.
KW FT PROPEP 23 45
KW FT PEPTIDE 46 72 .Omega-conotoxin CVID.
KW FT DISULFID 46 61 By similarity.
KW FT DISULFID 53 65 By similarity.
KW FT DISULFID 60 72 By similarity.
KW FT MOD_RES 72 72 Cysteine amide (G-73 provides amide
FT group).
SQ SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;

Query Match 51.7%; Score 62; DB 1; Length 73;
Best Local Similarity 30.4%; Pred. No. 41;
Matches 7; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXIXNQXCXQLDDCCSXCNXX 23
| : : : : : |
DB 46 CKSKGAKCKLMYDCGSGSGT 68

RESULT 72
Q646U3 PRELIMINARY; PRT; 74 AA.
ID AC Q646U3
AC Q646U3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RT Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723724; GAU21465.1; -
SQ SEQUENCE 74 AA; 7910 MW; C925922881E5EA3C CRC64;

Query Match 51.7%; Score 62; DB 2; Length 74;
Best Local Similarity 25.8%; Pred. No. 41;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

QY 2 XIXNQXCQ-----XLDCCSXCNXXNC 26
| : : : : : |
DB 41 KVTSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 73
Q646U4 PRELIMINARY; PRT; 74 AA.
ID AC Q646U4
AC Q646U4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.

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OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723723; AAU21464.1; -
SQ SEQUENCE 74 AA; 7879 MW; FF19FBA1F67B8A3E CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

QY 2 XIXNQXCXQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 74
Q646W2
ID Q646W2 PRELIMINARY; PRT; 74 AA.
AC Q646W2;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723704; AAU21445.1; -
SQ SEQUENCE 74 AA; 7807 MW; D9D10BA1F26FC5B0 CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

QY 2 XIXNQXCXQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 75
Q646W3
ID Q646W3 PRELIMINARY; PRT; 74 AA.
AC Q646W3;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AY723703; AAU21444.1; -
SQ SEQUENCE 74 AA; 7817 MW; 5373030B547B94FF CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

QY 2 XIXNQXCXQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 76
Q646W6
ID Q646W6 PRELIMINARY; PRT; 74 AA.
AC Q646W6;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DE Phytoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
RL Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723700; AAU21441.1; -
DR EMBL; AY723701; AAU21442.1; -
DR EMBL; AY723702; AAU21443.1; -
DR EMBL; AY723699; AAU21440.1; -
SQ SEQUENCE 74 AA; 7851 MW; D9D10BA1F67B94F1 CRC64;

Query Match
Best Local Similarity 51.7%; Score 62; DB 2; Length 74;
Matches 8; Conservative 14; Mismatches 3; Indels 6; Gaps 1;

QY 2 XIXNQXCXQ-----XLDCCSXXCNXXNC 26
Db 41 DVVSKCKKAINADPIAFHDCCKSCNTGSPC 71

RESULT 77
Q9AUD1
ID Q9AUD1 PRELIMINARY; PRT; 153 AA.
AC Q9AUD1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2S albumin.
OS Sesamum indicum (Oriental sesame) (Gingelly).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Lamiales; Pedaliaceae; Sesamum.
OX NCBI_TaxID=4182;
RN [1]
RP SEQUENCE FROM N.A.
RA Tai S.S.K., Lee T.T., Tsai C.C.Y., Yiu T.-J., Tzen J.T.C.;
RT "Expression pattern and deposition of three storage proteins, 11S
globulin, 2S albumin and 7S globulin in maturing sesame seeds.";
RL Plant Physiol. Biochem. 39:981-992(2001).
DR EMBL; AF240005; AAK15088.1; -
DR HSP; P01085; IHSS.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR000480; Glutelin.
DR InterPro; IPR000617; Napin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.

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DR PRINTS; PRO0211; GLUTELIN.
DR PRINTS; PRO0496; NAFIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 153 AA; 17504 MW; 6A8F9117DAE81568 CRC64;

Query Match 51.7%; Score 62; DB 2; Length 153;
Best Local Similarity 39.1%; Pred. No. 79;
Matches 9; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 4 XNQCXQXLDCCSCXXCNXXNC 26
Db 80 GNGQSEQLRDCQQLNVDERC 102

RESULT 78
EFL9 MOUSE
ID EFL9_MOUSE STANDARD; PRT; 382 AA.
AC Q8K1E3; Q9QVP3;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Multiple EGF-like-domain protein 9 precursor (Endothelial cell
DE specific protein S-1).
GN Name=Egfl9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.W., Green E.D., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 259-382 FROM N.A. (ISOFORM 2).
RA Fukudome K., Teuneyoshi N., Kimoto M.;
RT "Endothelial cell specific protein S-1."
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8K1E3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K1E3-2; Sequence=VSP_011768;
CC Note=No experimental confirmation available;
CC -1- SIMILARITY: Contains 6 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC

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CC EMBL; BC019431; AAH19431.1;
CC EMBL; AB011019; BAA8686.1; ALT_INIT.
CC HSP; P00750; ITPG.
CC MGD; MGI:2146838; Egfl9.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF_like.
CC Pfam; PF00008; EGF_5.
CC PRINTS; PR00010; EGFBL00D.
CC SMART; SM00179; EGF_CA; 2.
CC PROSITE; PS00010; ASX_HYDROXYL; 2.
CC PROSITE; PS00022; EGF_1; 6.
CC PROSITE; PS01186; EGF_2; 6.
CC PROSITE; PS50026; EGF_3; 6.
CC PROSITE; PS01187; EGF_CA; 2.
KW Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 382 Multiple EGF-like-domain protein 9.
FT DOMAIN 27 305 Extracellular (Potential).
FT TRANSMEM 306 326 Potential.
FT DOMAIN 327 382 Cytoplasmic (Potential).
FT DOMAIN 27 58 EGF-like 1.
FT DOMAIN 62 89 EGF-like 2.
FT DOMAIN 91 129 EGF-like 3.
FT DOMAIN 131 172 EGF-like 4.
FT DOMAIN 174 210 EGF-like 5, calcium-binding (Potential).
FT DOMAIN 212 248 EGF-like 6, calcium-binding (Potential).
FT DISULFID 29 40 By similarity.
FT DISULFID 33 46 By similarity.
FT DISULFID 48 57 By similarity.
FT DISULFID 66 71 By similarity.
FT DISULFID 79 88 By similarity.
FT DISULFID 95 107 By similarity.
FT DISULFID 101 117 By similarity.
FT DISULFID 119 128 By similarity.
FT DISULFID 135 148 By similarity.
FT DISULFID 142 160 By similarity.
FT DISULFID 162 171 By similarity.
FT DISULFID 178 189 By similarity.
FT DISULFID 183 198 By similarity.
FT DISULFID 200 209 By similarity.
FT DISULFID 216 227 By similarity.
FT DISULFID 221 236 By similarity.
FT DISULFID 238 247 By similarity.
FT CARBOHYD 157 157 Missing (in isoform 2).
FT VARSPPLIC 295 311 /FTId=VSP_011768.
SQ SEQUENCE 382 AA; 40404 MW; F2C82AD649CA0B3C CRC64;

Query Match 51.7%; Score 62; DB 1; Length 382;
Best Local Similarity 32.0%; Pred. No. 1.8e+02;
Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 2 XIXNQXCXQXLDCCSCXXCNXXNC 26
Db 203 GFAGREFTINLDDCASRRCQRC 227

RESULT 79
EFL9 HUMAN
ID EFL9_HUMAN STANDARD; PRT; 383 AA.
AC Q6UY11; Q9B054;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Multiple EGF-like-domain protein 9 precursor (UNQ2903/PRO28633).
GN Name=EgFL9;
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RX SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
 RA Vandlen R., Watanabe C., Weiland D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Name=1;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=2;
 CC IsoId=Q6UY11-1; Sequence=Displayed;
 CC Note=Splicing acceptor site not canonical. No experimental
 CC confirmation available;
 CC IsoId=Q6UY11-2; Sequence=VSP_011767;
 CC Note=Splicing acceptor site not canonical. No experimental
 CC confirmation available;
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AV358126; AAQ88493.1; -;
 CC EMBL; BC000230; AAH00230.1; -;
 CC EMBL; BC006425; AAH06425.1; -;
 CC Genbank; HGNC:21113; EGF_L9.
 DR InterPro; IPR000152; Asx hydroxyl S.
 DR InterPro; IPR008985; ConA like_1ec_g1.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.

DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00008; EGF_5.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00181; EGF_6.
 DR SMART; SM00179; EGF_CA; 4.
 DR PROSITE; PS00010; ASX HYDROXYL; 2.
 DR PROSITE; PS00022; EGF_1; 6.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS00026; EGF_3; 6.
 DR PROSITE; PS01187; EGF_CA; 2.
 KW Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26 Potential.
 FT CHAIN 27 383 Multiple EGF-like-domain protein 9.
 FT DOMAIN 27 306 Extracellular (Potential).
 FT TRANSMEM 307 327 Potential.
 FT DOMAIN 328 383 Cytoplasmic (Potential).
 FT DOMAIN 27 58 EGF-like 1.
 FT DOMAIN 62 89 EGF-like 2.
 FT DOMAIN 91 129 EGF-like 3.
 FT DOMAIN 131 172 EGF-like 4.
 FT DOMAIN 174 210 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN 212 248 EGF-like 6, calcium-binding (Potential).
 FT DISULFID 29 40 By similarity.
 FT DISULFID 33 46 By similarity.
 FT DISULFID 48 57 By similarity.
 FT DISULFID 66 71 By similarity.
 FT DISULFID 79 88 By similarity.
 FT DISULFID 95 107 By similarity.
 FT DISULFID 101 117 By similarity.
 FT DISULFID 119 128 By similarity.
 FT DISULFID 135 148 By similarity.
 FT DISULFID 142 160 By similarity.
 FT DISULFID 162 171 By similarity.
 FT DISULFID 178 189 By similarity.
 FT DISULFID 193 198 By similarity.
 FT DISULFID 200 209 By similarity.
 FT DISULFID 216 227 By similarity.
 FT DISULFID 221 236 By similarity.
 FT DISULFID 238 247 By similarity.
 FT CARBOHYD 157 157 N-linked (GlcNAc...) (Potential).
 FT VARSPPLIC 1 179 Missing (in isoform 2).
 FT /FTid=VSP_011767;
 SQ SEQUENCE 383 AA; 40547 MW; 701AC6B043863EA7 CRC64;
 Query Match 51.7%; Score 62; DB 1; Length 383;
 Best Local Similarity 32.0%; Pred. No. 1.8e+02;
 Matches 8; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 OY 2 XIXNQXCXQLDDCCSXCNXNC 26
 Db 203 GFAGFCTINLDDCASRPCQGARC 227
 RESULT 80
 Q7PM27 PRELIMINARY; PRT; 638 AA.
 ID Q7PM27 AC Q7PM27; 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE ENSANGP0000014402 (Fragment).
 GN Name=ENSANGG0000011913;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

DR EMBL; AAB01008980; EAA14483.2; --
DR HSP; P19438; 1EXT.
DR InterPro; IPR003341; DUF139.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF02363; Ctriplex; 15.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS01186; EGF_2; 4.
FT NON TER 1
FT NON TER 638
SQ SEQUENCE 638 AA; 69390 MW; 026DB44846AB483F CRC64;

Query Match 51.7%; Score 62; DB 2; Length 638;

Best Local Similarity 28.0%; Pred. No. 2.9e+02;

Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXCNXNKC 26

DB 30 RLSNHRICPHCDCCDNGICTKPGYC 54

RESULT 81

ID Q962W9 PRELIMINARY; PRT; 713 AA.

AC Q962W9;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE EGF-like protein (Fragment).

OS Podocoryne carnea.

OC Eukaryota; Metazoa; Chnidaria; Hydrozoa; Hydroids; Anthomedusae;

OC Hydrocnididae; Podocoryne.

OX NCBI_TaxID=6096;

RN [1]

RP SEQUENCE FROM N.A.

RA Bauer P., Plickert G.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF397902; AAK92130.1; --

DR HSP; P00740; 1EDM.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR InterPro; IPR00152; Asx_hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR Pfam; PF00008; EGF; 18.

DR PRINTS; PR00010; EGFBLD.

DR SMART; SM00179; EGF_CA; 16.

DR PROSITE; PS00010; ASX_HYDROXYL; 17.

DR PROSITE; PS00022; EGF_1; 18.

DR PROSITE; PS01186; EGF_2; 18.

DR PROSITE; PS50026; EGF_3; 18.

DR PROSITE; PS01187; EGF_CA; 16.

DR EGF-like domain.

FT NON TER 1

SQ SEQUENCE 713 AA; 76908 MW; 980E392B533E42D0 CRC64;

Query Match 51.7%; Score 62; DB 2; Length 713;

Best Local Similarity 26.9%; Pred. No. 3.2e+02;

Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;

OY 2 XIXNQXCXQLDDCCSXCNXNKC 27

DB 489 GFTGETCEIIDECSSPCCQAGTCV 514

RESULT 82

ID_DLL1 RAT

AC P97677; STANDARD; PRT; 714 AA.

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
GN Names=Dll1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Disibio G., Hebshi L., Boulter J., Weinmaster G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May be involved in cell-to-cell communication in
mammalian embryos. May have a role in cellular interactions
underlying somitogenesis and development of the nervous system (By
similarity).
CC -1- SUBUNIT: Interacts with Notch receptors.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 1 DSL domain.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC EMBL; U78889; AAB37343.1; --
DR HSP; P08709; 1BP9.
DR GO; 70949; Dll1.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005112; F:Notch binding; IPI.
DR GO; GO:0030154; P:cell differentiation; ISS.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0009912; P:hair cell fate commitment; NAS.
DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
DR GO; GO:0007399; P:neurogenesis; NAS.
DR GO; GO:0007219; P:Notch signaling pathway; NAS.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBLD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS50026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 714
FT DOMAIN 18 537
FT TRANSMEM 538 560
FT DOMAIN 561 714
FT DOMAIN 158 220
FT DOMAIN 225 253
FT DOMAIN 256 284
FT DOMAIN 291 324
FT DOMAIN 331 362
FT DOMAIN 369 401

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FT DOMAIN 408 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7, calcium-binding (Potential).
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
FT DISULFID 229 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 256 267 By similarity.
FT DISULFID 262 273 By similarity.
FT DISULFID 275 284 By similarity.
FT DISULFID 291 303 By similarity.
FT DISULFID 297 313 By similarity.
FT DISULFID 315 324 By similarity.
FT DISULFID 331 342 By similarity.
FT DISULFID 336 351 By similarity.
FT DISULFID 353 362 By similarity.
FT DISULFID 369 380 By similarity.
FT DISULFID 374 390 By similarity.
FT DISULFID 392 401 By similarity.
FT DISULFID 408 419 By similarity.
FT DISULFID 413 428 By similarity.
FT DISULFID 430 439 By similarity.
FT DISULFID 446 466 By similarity.
FT DISULFID 468 477 By similarity.
FT DISULFID 484 495 By similarity.
FT DISULFID 489 504 By similarity.
FT DISULFID 506 515 By similarity.
FT CARBOHYD 476 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 714 AA; 77378 MW; 4B8EE2272BAEA27E CRC64;

Query Match 51.7%; Score 62; DB 1; Length 714;
Best Local Similarity 28.0%; Pred. No. 3.2e+02;
Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

QY 2 XIXNQXQXLDCCSXXCNXXNC 26
Db 433 GFGRYCEDNVDCCASSPCANGGTC 457

RESULT 83
ID D1L1_MOUSE STANDARD; PRT; 722 AA.
AC Q61483;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Deltal).
GN Name=D1L1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X BALB/c; TISSUE=Embryo;
RX MEDLINE=95401858; PubMed=7671806;
RA Bettenhausen B., de Angelis M.H., Simon D., Guenet J.-L., Gossler A.;
RT "Transient and restricted expression during mouse embryogenesis of
RL D1L1, a murine gene closely related to Drosophila Delta.";
RL Development 121:2407-2418(1995).
CC -!- FUNCTION: May be involved in cell-to-cell communication in
CC mammalian embryos. May have a role in cellular interactions
CC underlying somitogenesis and development of the nervous system.
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: In the embryo, expressed in the paraxial
CC mesoderm and nervous system. Expressed at high levels in adult
CC heart and at lower levels, in adult lung.
CC -!- DEVELOPMENTAL STAGE: Expressed until day 15 in the embryo.
CC Expression then decreases and increases again in the adult.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80903; CAA56865.1; -.
DR PIR; I48324; I48324.
DR HSP; P00740; IEDM.
DR IntAct; Q61483; -.
DR MGD; MGI:104659; D1L1.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0005887; C:integral to plasma membrane; ISS.
DR GO; GO:0005112; F:protein binding; IPI.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0007386; P:compartment specification; ISS.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
DR GO; GO:0009912; P:hair cell fate commitment; NAS.
DR GO; GO:0030097; P:hemopoiesis; ISS.
DR GO; GO:0042472; P:inner ear morphogenesis; NAS.
DR GO; GO:0007399; P:neurogenesis; NAS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); NAS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFLOOD.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17 Potential.
FT CHAIN 18 722 Delta-like protein 1.
FT DOMAIN 18 545 Extracellular (Potential).
FT TRANSMEM 546 568 Potential.
FT DOMAIN 569 722 Cytoplasmic (Potential).
FT DOMAIN 158 220 DSL.
FT DOMAIN 225 253 EGF-like 1.
FT DOMAIN 256 284 EGF-like 2.
FT DOMAIN 291 324 EGF-like 3.
FT DOMAIN 331 362 EGF-like 4, calcium-binding (Potential).
FT DOMAIN 369 401 EGF-like 5.
FT DOMAIN 408 439 EGF-like 6.
FT DOMAIN 446 477 EGF-like 7.
FT DOMAIN 484 515 EGF-like 8.
FT DISULFID 225 236 By similarity.
FT DISULFID 229 242 By similarity.
FT DISULFID 244 253 By similarity.
FT DISULFID 256 267 By similarity.
FT DISULFID 262 273 By similarity.
FT DISULFID 275 284 By similarity.
FT DISULFID 291 303 By similarity.
FT DISULFID 297 313 By similarity.
FT DISULFID 315 324 By similarity.
FT DISULFID 331 342 By similarity.
FT DISULFID 336 351 By similarity.
FT DISULFID 353 362 By similarity.
FT DISULFID 369 380 By similarity.
FT DISULFID 374 390 By similarity.
FT DISULFID 392 401 By similarity.
FT DISULFID 408 419 By similarity.

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RC STRAIN=C57BL/6J;
RA Brattwatt M., Waeltz P., Dudekta D., Nagaraja R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 8 EGF-like domains.
DR ENBL; BC057400; AAH57400.1; -
DR ENBL; BC065063; AAH65063.1; -
DR ENBL; AY497019; AAR30869.1; -
DR HSSP; P00743; IAP0.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0007368; P:determination of left/right symmetry; IMP.
DR GO; GO:0001757; P:somite specification; IMP.
DR InterPro; IPRO00152; ASx_hydroxyl_S.
DR InterPro; IPRO01774; DSL_
DR InterPro; IPRO00742; EGF_2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO01438; EGF-II.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO06210; IEFGF.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PRO00010; EGFBLOOD.
DR SMART; SM00051; DSL; 1.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF_CA; 6.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 6.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 722 AA; 78449 MW; 9D570B9DC7EEC75E CRC64;

Query Match 51.7%; Score 62; DB 2; Length 722;
Best Local Similarity 28.0%; Pred.No. 3.2e+02;
Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps:

Qy 2 XIXNXOXCXXLDCCSXCNKXNC 26
Db 433 GFSGRYCEDNDDCASSPCANGGTC 457
:::|||||:::|:::|

RESULT 85
DLL1_HUMAN STANDARD; PRT; 723 AA.
AC 000548; Q9NU41; Q9UUV2;
CT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).
DE (H-Delta-1) (UNQ146/PRO172).
GN Name=DLL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.B., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
RA Banks A., Leaman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.
RT "Human ligands of the Notch receptor."
RL Am. J. Pathol. 154:785-794 (1999).
RL [2]
RN SEQUENCE FROM N.A.
RP Han W., Ye Q., Moore M.A.S.;
RT "A soluble form of human delta-like-1 inhibits differentiation of
RT hematopoietic progenitor cells."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A.

```

RA Oda T., Chandrasekharappa S.C.;
RT "Human Delta 1 gene sequence";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBSJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Haas P.E., Heldens S.,
RA Huang A., Kim H.S., Klinowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment";
RL Genome Res. 13:2265-2270(2003).
RN [5]
RP SEQUENCE FROM N.A.
RX Almeida J.;
RA Submitted (APR-2000) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP FUNCTION:
RX MEDLINE=21464863; PubMed=11581320;
RA Jaleco A.C., Neves H., Hooijberg E., Gameiro P., Clode N., Haury M.,
RA Henrique D., Parreira L.;
RA "Differential effects of Notch ligands Delta-1 and Jagged-1 in human
RA lymphoid differentiation";
RT J. Exp. Med. 194:991-1001(2001).
RN [7]
RP FUNCTION: Acts as a ligand for Notch receptors. Blocks the
RP differentiation of progenitor cells into the B-cell lineage while
RP promoting the emergence of a population of cells with the
RP characteristics of a T-cell/NK-cell precursor.
CC -!- SUBUNIT: Interacts with Notch receptors.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in heart and pancreas, with lower
CC expression in brain and muscle and almost no expression in
CC placenta, lung, liver, and kidney.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 8 EGF-like domains.
CC -----
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CC -----
DR EMBL; AF003522; AB61286.1; -
DR EMBL; AF196571; AA05834.1; -
DR EMBL; AF222310; AAQ09716.1; -
DR EMBL; AY358892; AAQ89251.1; -
DR EMBL; AL078605; CAB89569.1; -
DR HSSP; P00740; 1EDM.
DR Genew; HGNC:2908; DLL1.
DR MTM; 60582; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0005112; F:Notch binding; IPI.
DR GO; GO:0030154; P:cell fate differentiation; TAS.
DR GO; GO:0001709; P:cell fate determination; NAS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0005912; P:hair cell fate commitment; ISS.
DR GO; GO:0030097; P:hemopoiesis; NAS.
DR GO; GO:0042472; P:inner ear morphogenesis; ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; NAS.
DR GO; GO:0042475; P:odontogenesis (sensu Vertebrata); ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; TAS.
InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 6.
DR PRINTS; PR00010; EGFBL00D.
DR SMART; SM0051; DSL; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 8.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 1.
KW Developmental protein; Differentiation; EGF-like domain; Glycoprotein;
KW Notch signaling pathway; Repeat; Signal; Transmembrane.
FT SIGNAL 1 17
FT CHAIN 18 723
FT DOMAIN 18 545
FT TRANSMEM 546 568
FT DOMAIN 569 723
FT DOMAIN 159 221
FT DOMAIN 226 254
FT DOMAIN 257 285
FT DOMAIN 292 325
FT DOMAIN 332 363
FT DOMAIN 370 402
FT DOMAIN 409 440
FT DOMAIN 447 478
FT DOMAIN 485 516
FT DISULFID 226 237
FT DISULFID 230 243
FT DISULFID 245 254
FT DISULFID 257 268
FT DISULFID 263 274
FT DISULFID 276 285
FT DISULFID 292 304
FT DISULFID 298 314
FT DISULFID 316 325
FT DISULFID 332 343
FT DISULFID 337 352
FT DISULFID 354 363
FT DISULFID 370 381
FT DISULFID 375 391
FT DISULFID 393 402
FT DISULFID 409 420
FT DISULFID 414 429
FT DISULFID 431 440
FT DISULFID 447 467
FT DISULFID 469 478
FT DISULFID 485 496
FT DISULFID 490 505
FT DISULFID 507 516
FT CARBOHYD 477 477
FT CONFLICT 498 498
FT CONFLICT 502 502
FT CONFLICT 510 510
SQ SEQUENCE 723 AA; 77956 MW; B4EC455FFA32A12B CRC64;
Query Match 51.7%; Score 62; DB 1; Length 723;
Best Local Similarity 28.0%; Pred. No. 3.3e+02;
Matches 7; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
Oy 2 XIXNQXCXQXLDCCSXCNXNKC 26
Db 434 GFSGRHCDNDVDCASSPCANGTC 458
RESULT 86
Q66S04
ID Q66S04 PRELIMINARY; PRT; 824 AA.
AC Q66S04;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Notch receptor-like protein.
 GN ORFNames=008-50;
 OS Oikopleura dioica.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
 OC Oikopleuridae; Oikopleura.
 OX NCBI_TaxID=34765;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=1534333; DOI=10.1038/nature02709;
 RA Sso H.C., Edvardson R.B., Maeland A.D., Bjordal M., Jensen M.F.,
 RA Hansen A., Flaot M., Weissenbach J., Lehrach H., Wincker P.,
 RA Reinhardt R., Chourrout D.;
 RT "Hex cluster integration with persistent anteroposterior order of
 RT expression in Oikopleura dioica";
 RL Nature 431:67-71(2004)
 DR EMBL; AY613856; AY47887.1; -;
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF; 11.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00181; EGF; 17.
 DR SMART; SM00179; EGF CA; 15.
 DR PROSITE; PS00010; ASX_HYDROXYL; 10.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 17.
 DR PROSITE; PS01186; EGF_2; 14.
 DR PROSITE; PS00026; EGF_3; 2.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor.
 SQ SEQUENCE 824 AA; 89253 MW; 955AEAE53CFC86A CRC64;
 Query Match 51.78; Score 62; DB 2; Length 824;
 Best Local Similarity 30.88; Pred. No. 3.7e+02;
 Matches 8; Conservative 12; Mismatches 6; Indels 0; Gaps 0;
 QY 1 CXIXNOXCXQXLDQCCSXCNXXNXC 26
 Db 154 CELEKSFCEQFPNYCENGDCNDGGPC 179
 RESULT 87
 FBPI STRPU STANDARD; PRT; 1064 AA.
 AC P10079;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Fibropellin I precursor (Epidermal growth factor-related protein 1)
 DE (UEGF-1)
 GN Name=EGF1;
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90112459; PubMed=25114273;
 RA Delgadillo-Reynoso M.G., Rollo D.R., Hursh D.A., Raff R.A.;
 RT "Structural analysis of the uEGF gene in the sea urchin
 RT strongylocentrotus purpuratus reveals more similarity to vertebrate
 RT than to invertebrate genes with EGF-like repeats.";
 RL J. Mol. Evol. 29:314-327(1989).
 RN [2]

RP SEQUENCE OF 279-476 AND 781-1064 FROM N.A.
 RX MEDLINE=87319677; PubMed=3498216;
 RA Hursh D.A., Andrews M.E., Raff R.A.;
 RT "A sea urchin gene encodes a polypeptide homologous to epidermal
 RT growth factor";
 RL Science 237:1487-1490(1987).
 RN [3]
 RP AVIDIN-LIKE DOMAIN.
 RX MEDLINE=89196806; PubMed=2784773;
 RA Hunt L.T., Barker W.C.;
 RT "Avidin-like domain in an epidermal growth factor homolog from a sea
 RT urchin";
 RL FASEB J. 3:1760-1764(1989).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=91285254; PubMed=2060714;
 RA Bisgrove B.W., Andrews M.E., Raff R.A.;
 RT "Fibropellins, products of an EGF repeat-containing gene, form a
 RT unique extracellular matrix structure that surrounds the sea urchin
 RT embryo";
 RL Dev. Biol. 146:89-99(1991).
 CC -I- FUNCTION: Forms the apical lamina, a component of the
 CC extracellular matrix.
 CC -I- SUBCELLULAR LOCATION: Extracellular. In vesicles in the cytoplasm
 CC of unfertilized eggs, then to the base of the hyalin layer
 CC throughout development and finally in the apical lamina in late
 CC embryos and early larvae.
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=IA;
 CC IsoId=P10079-1; Sequence=Displayed;
 CC Name=IB;
 CC IsoId=P10079-2; Sequence=VSP_000451;
 CC -I- DEVELOPMENTAL STAGE: Moderate levels in unfertilized eggs and
 CC during early cleavage, then rapidly increases in abundance between
 CC late morula and mesenchyme blastula stages to maximal levels
 CC maintained through subsequent stages. Expressed both maternally
 CC and zygotically.
 CC -I- SIMILARITY: Contains 1 avidin domain.
 CC -I- SIMILARITY: Contains 1 CUB domain.
 CC -I- SIMILARITY: Contains 21 EGF-like domains.
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 CC EMBL; L08692; AAA62164.1; -;
 DR EMBL; L08692; AAA62163.1; -;
 DR EMBL; X17530; CAA35571.1; -;
 DR EMBL; M17421; CAA30050.1; -;
 DR EMBL; X17533; CAA35573.1; -;
 DR PIR; A40136; A40136.
 DR HSSP; P01132; 1EGF.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR005469; Avidin.
 DR InterPro; IPR005468; Avidin/str.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF01382; Avidin; 1.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 21.
 DR PRINTS; PR00709; AVIDIN.
 DR PRINTS; PR00010; EGFBL00D.
 DR PROSITE; PS00010; ASX_HYDROXYL; 19.
 DR PROSITE; PS00577; AVIDIN; 1.
 DR PROSITE; PS01180; CUB; 1.

DR PROSITE; PS00022; EGF 1; 19.
 DR PROSITE; PS01186; EGF 2; 19.
 DR PROSITE; PS00026; EGF 3; 21.
 DR PROSITE; PS01187; EGF-Ca; 18.
 KW Alternative splicing; Biotin; Calcium-binding; EGF-like domain;
 KW Glycoprotein; Repeat; Signal.
 FT CHAIN 1 19 Potential.
 FT SIGNAL 20 1064 Fibropellin I.
 FT DOMAIN 20 55 EGF-like 1.
 FT DOMAIN 62 175 CUB.
 FT DOMAIN 176 212 EGF-like 2, calcium-binding (Potential).
 FT DOMAIN 214 250 EGF-like 3, calcium-binding (Potential).
 FT DOMAIN 252 288 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 290 326 EGF-like 5, calcium-binding (Potential).
 FT DOMAIN 328 364 EGF-like 6, calcium-binding (Potential).
 FT DOMAIN 366 402 EGF-like 7, calcium-binding (Potential).
 FT DOMAIN 404 440 EGF-like 8, calcium-binding (Potential).
 FT DOMAIN 442 478 EGF-like 9, calcium-binding (Potential).
 FT DOMAIN 480 516 EGF-like 10, calcium-binding (Potential).
 FT DOMAIN 518 554 EGF-like 11, calcium-binding (Potential).
 FT DOMAIN 556 592 EGF-like 12, calcium-binding (Potential).
 FT DOMAIN 594 630 EGF-like 13, calcium-binding (Potential).
 FT DOMAIN 632 668 EGF-like 14, calcium-binding (Potential).
 FT DOMAIN 670 706 EGF-like 15, calcium-binding (Potential).
 FT DOMAIN 708 746 EGF-like 16, calcium-binding (Potential).
 FT DOMAIN 748 782 EGF-like 17, calcium-binding (Potential).
 FT DOMAIN 822 858 EGF-like 18, calcium-binding (Potential).
 FT DOMAIN 860 896 EGF-like 19, calcium-binding (Potential).
 FT DOMAIN 898 934 EGF-like 20, calcium-binding (Potential).
 FT DOMAIN 936 1064 EGF-like 21, calcium-binding (Potential).
 FT DISULFID 23 34 Avidin.
 FT DISULFID 28 43 By similarity.
 FT DISULFID 45 54 By similarity.
 FT DISULFID 180 191 By similarity.
 FT DISULFID 185 200 By similarity.
 FT DISULFID 202 211 By similarity.
 FT DISULFID 218 229 By similarity.
 FT DISULFID 223 238 By similarity.
 FT DISULFID 240 249 By similarity.
 FT DISULFID 256 267 By similarity.
 FT DISULFID 261 276 By similarity.
 FT DISULFID 278 287 By similarity.
 FT DISULFID 294 305 By similarity.
 FT DISULFID 299 314 By similarity.
 FT DISULFID 316 325 By similarity.
 FT DISULFID 332 343 By similarity.
 FT DISULFID 337 352 By similarity.
 FT DISULFID 354 363 By similarity.
 FT DISULFID 370 381 By similarity.
 FT DISULFID 375 390 By similarity.
 FT DISULFID 392 401 By similarity.
 FT DISULFID 408 419 By similarity.
 FT DISULFID 413 428 By similarity.
 FT DISULFID 430 439 By similarity.
 FT DISULFID 446 457 By similarity.
 FT DISULFID 451 466 By similarity.
 FT DISULFID 468 477 By similarity.
 FT DISULFID 484 495 By similarity.
 FT DISULFID 489 504 By similarity.
 FT DISULFID 506 515 By similarity.
 FT DISULFID 522 533 By similarity.
 FT DISULFID 527 542 By similarity.
 FT DISULFID 544 553 By similarity.
 FT DISULFID 560 571 By similarity.
 FT DISULFID 565 580 By similarity.
 FT DISULFID 582 591 By similarity.
 FT DISULFID 598 609 By similarity.
 FT DISULFID 603 618 By similarity.
 FT DISULFID 620 629 By similarity.
 FT DISULFID 636 647 By similarity.
 FT DISULFID 641 656 By similarity.
 FT DISULFID 658 667 By similarity.

FT DISULFID 674 685 By similarity.
 FT DISULFID 679 694 By similarity.
 FT DISULFID 696 705 By similarity.
 FT DISULFID 712 723 By similarity.
 FT DISULFID 717 732 By similarity.
 FT DISULFID 734 743 By similarity.
 FT DISULFID 750 761 By similarity.
 FT DISULFID 755 770 By similarity.
 FT DISULFID 772 781 By similarity.
 FT DISULFID 788 799 By similarity.
 FT DISULFID 793 808 By similarity.
 FT DISULFID 810 819 By similarity.
 FT DISULFID 826 837 By similarity.
 FT DISULFID 831 846 By similarity.
 FT DISULFID 848 857 By similarity.
 FT DISULFID 864 875 By similarity.
 FT DISULFID 869 884 By similarity.
 FT DISULFID 886 895 By similarity.
 FT DISULFID 902 913 By similarity.
 FT DISULFID 907 922 By similarity.
 FT DISULFID 924 933 By similarity.
 FT CARBOHYD 30 30 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 851 851 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 477 780 Missing (in isoform IB).
 FT CONFLICT 279 279 /FTid=VSP_000451.
 FT SEQUENCE 1064 AA; 112072 MW; 2E569CA012ED6D09 CRC64;
 SQ
 Query Match 51.7%; Score 62; DB 1; Length 1064;
 Best Local Similarity 26.9%; Pred. No. 4.6e+02;
 Matches 7; Conservative 13; Mismatches 6; Indels 0; Gaps 0;
 QY 2 XIXNXXCXQLDDCCSXXCNXXNXC 27
 Db 205 GFTGRNCIDIDECASDPQNGACV 230
 RESULT 88
 Q7QCT2 PRELIMINARY; PRT; 1286 AA.
 ID Q7QCT2
 AC Q7QCT2
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE AGCP1804 (Fragment).
 GN Name=sgCGS1928; ORFNames=ENSANGG00000014325;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PEST;
 RA Anopheles Genome Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB01008859; EAA07783.1; -.
 DR HSP; P00740; IEDM.
 DR GO; GO:0005509; F:Calcium ion binding; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR008985; ConA_like_lcc_gl.
 DR InterPro; IPR006207; Cys_knot_C.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000372; LRR_Nterm.

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DR InterPro; IPR003591; LRR_typ.
DR Pfam; PFO00008; EGF_7.
DR Pfam; PFO1463; LRRCT; 4.
DR Pfam; PFO1462; LRRNT; 3.
DR Pfam; PFO0560; LRR_1; 14.
DR Pfam; PFO0560; LRR_1; 14.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00019; LEURICHRPT.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS01185; CTCK_1; 1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 7.
DR PROSITE; PS00022; EGF_1; 7.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G DOMAIN; 1.
DR PROSITE; PS00119; PA2_ASP; UNKNOWN_1.
KW EGF-like domain.
FT NON_TER 1
SQ SEQUENCE 1286 AA; 144156 MW; E919D876B21BB3E CRC64;

Query Match 51.7%; Score 62; DB 2; Length 1286;
Best Local Similarity 33.3%; Pred. No. 5.5e+02;
Matches 7; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 7 XCXQXLDCCSXCNXXNCV 27
: : : : : : : : : : : : : : : :
Db 882 NCTDNIDDCVNHMCQNGGTCV 902

RESULT 89
Q9DE37
ID Q9DE37 PRELIMINARY; PRT; 1515 AA.
AC Q9DE37;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Slit3.
GN Names=slit3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Michigan;
RX MEDLINE=21098742; PubMed=11161558; DOI=10.1006/dbio.2000.0105;
RA Yeo S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C.,
RA Kuwada J.Y., Huh T.L., Okamoto H.;
RT "Overexpression of a slit homologue impairs convergent extension of
RT the mesoderm and causes cyclopia in embryonic zebrafish.";
RL Dev. Biol. 230:1-17(2001).
DR EMBL; AF210320; AAC36772.1; -.
DR HSP; P01132; 1GKS.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx hydroxyl S.
DR InterPro; IPR006207; Cys knot C.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003645; Fol_N.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_typ.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PFO0008; EGF_7.
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DR Pfam; PFO2210; Laminin_G_2; 1.
DR Pfam; PFO1463; LRRCT; 4.
DR Pfam; PFO1462; LRRNT; 4.
DR Pfam; PFO0560; LRR_1; 19.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00282; LAMG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR SMART; SM00369; LRR_TYP; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 8.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G DOMAIN; 1.
KW EGF-like domain.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD111277D18D5B CRC64;

Query Match 51.7%; Score 62; DB 2; Length 1515;
Best Local Similarity 33.3%; Pred. No. 6.4e+02;
Matches 8; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 4 XNQCXQXLDCCSXCNXXNCV 27
: : : : : : : : : : : : : : : :
Db 1059 VQCCQEQDYNDCLNKCQHGACV 1082

RESULT 90
Q9U4A2
ID Q9U4A2 PRELIMINARY; PRT; 1685 AA.
AC Q9U4A2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Variant surface protein PfEMP1 (Fragment).
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
RA Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T.,
RA Pinches R., Baruch D.I., Newbold C.I., Miller L.H.;
RT "Identification of a Plasmodium falciparum intercellular adhesion
RT molecule-1 binding domain: a parasite adhesion trait implicated in
RT cerebral malaria.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1766-1771(2000).
DR EMBL; AF193424; AAF18980.1; -.
DR GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR000454; Eub ATPase_Csub.
DR InterPro; IPR004258; PEEMP.
DR Pfam; PFO3011; PFEMP; 1.
DR PROSITE; PS00605; ATPASE_C; UNKNOWN_1.
FT NON_TER 1685
SQ SEQUENCE 1685 AA; 193671 MW; D1FD426666B0551E CRC64;

Query Match 51.7%; Score 62; DB 2; Length 1685;
Best Local Similarity 29.6%; Pred. No. 7e+02;
Matches 8; Conservative 13; Mismatches 4; Indels 2; Gaps 1;

QY 1 CXIXNQXQXQXLDCC--CSXCNXXNX 25
: : : : : : : : : : : : : : : :
Db 1048 CXTKDKCKTCKSDCCNTCTEACTAYNR 1074

RESULT 91
```

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.


```

CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -I- SIMILARITY: Belongs to the mu-agatoxin family.
DR PIR: A32038; A32038.
DR PDB: 1E1T; NMR: @=1-36.
DR InterPro: IPR009243; Toxin 7.
DR Pfam: PF05980; Toxin_7; 1.
DR KMW 3D-structure; Amidation; Direct protein sequencing; Neurotoxin; Toxin.
FT FT DISULFID 2 17
FT FT DISULFID 9 22
FT FT DISULFID 16 32
FT FT DISULFID 24 30
FT FT MOD_RES 36 36 Asparagine amide.
FT FT STRAND 3 3
FT FT TURN 5 6
FT FT STRAND 16 16
FT FT TURN 18 19
FT FT STRAND 20 26
FT FT TURN 27 28
FT FT STRAND 29 34
SQ SEQUENCE 36 AA; 4273 MW; 3B973A605B90DE85 CRC64;

Query Match 51.2%; Score 61.5; DB 1; Length 36;
Best Local Similarity 26.7%; Pred. No. 24;
Matches 8; Conservative 12; Mismatches 7; Indels 3; Gaps 1;

QY 1 CXIXNXXCXQLDDCCS---XXGNXXNXCV 27
| : : : : : : : : : : : : : : : : : :
Db 2 CVPENGHCRDWYDECCEGFCYSCRCQPPKCI 31

RESULT 95
Q9BP77 PRELIMINARY; PRT; 81 AA.
AC Q9BP77;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Conotoxin scaffold VI/VII.
OS Conus atenatus (Sand-dusted cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=89451;
RN NCBI_TaxID=89451;
RP [1]
RZ SEQUENCE FROM N.A.
RX MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G.; Gildad Y.; Avidan N.; Ben-Asher E.; Levy Z.;
RA Fainzilber M.;
RT "Mechanisms for evolving hypervariability: the case of conopeptides.";
RL Mol. Biol. Evol. 18:130-131(2001).
DR EMEL: AF215061; AAG60489.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR004214; Conotoxin.
DR Pfam: PF02950; Conotoxin; 1.
DR SQ SEQUENCE 81 AA; 8697 MW; 99EB0139D26851D5 CRC64;

Query Match 51.2%; Score 61.5; DB 2; Length 81;
Best Local Similarity 27.6%; Pred. No. 50;
Matches 8; Conservative 12; Mismatches 6; Indels 3; Gaps 1;

QY 1 CXIXNXXCXQLDDCCSXXC---NXXNXC 26
| : : : : : : : : : : : : : : : : : :
Db 46 CTVDSDCPDNNHDCSCRIDEGGSGVC 74

RESULT 96
Q8LAG1 PRELIMINARY; PRT; 471 AA.
ID Q8LAG1
AC Q8LAG1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)

```

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22088475; PubMed=12093376;
 RA Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087835; AAM65388.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 53428 MW; 3573C789C54FB28A CRC64;

Query Match 51.2%; Score 61.5; DB 2; Length 471;
 Best Local Similarity 22.2%; Pred. No. 2.5e+02;
 Matches 8; Conservative 12; Mismatches 7; Indels 9; Gaps 1;

QY 1 CXIXNQXCXQLDCC-----CSXXCNXKVCV 27
 DB 150 CKAGNEKRSIMPQCEATLPAMPDCICGGERKFCV 185

RESULT 97
 Q8VZE5
 ID Q8VZE5 PRELIMINARY; PRT; 471 AA.
 AC Q8VZE5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Atlg05410/T25N20_5 (Hypothetical protein Atlg05410).
 GN Name=Atlg05410;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesena E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
 RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.

RA Kim C.J., Chen H., Cheuk R., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Davis R.W., Theologis A., Ecker J.R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY065014; AAL57658.1; -;
 DR EMBL; AY074502; AAL69486.1; -;
 DR EMBL; AY096601; AAM20251.1; -;
 DR EMBL; AY142043; AAM98307.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 471 AA; 53368 MW; 582512E495010DDA CRC64;

Query Match 51.2%; Score 61.5; DB 2; Length 471;
 Best Local Similarity 22.2%; Pred. No. 2.5e+02;
 Matches 8; Conservative 12; Mismatches 7; Indels 9; Gaps 1;

QY 1 CXIXNQXCXQLDCC-----CSXXCNXKVCV 27
 DB 150 CKAGNEKRSIMPQCEATLPAMPDCICGGERKFCV 185

RESULT 98
 Q9ZVZ7
 ID Q9ZVZ7 PRELIMINARY; PRT; 481 AA.
 AC Q9ZVZ7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE T25N20.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Johnson-Hopson C., Brooks S., Buehler E., Chao Q., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
 RA Ecker J.R.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

RP SEQUENCE FROM N.A.
RX MEDLINE=94150815; PubMed=8107968; DOI=10.1016/0028-3908(93)90008-Q;
RA Monje V.D., Haack J.A., Naisbitt S.R., Miljanich G., Ramachandran J.,

Search completed: April 18, 2005, 20:37:46
Job time : 121 secs

Search completed: April 18, 2005, 20:37:46
Job time : 121 secs

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GenCore version S.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 19:58:50 ; Search time 125 Seconds
(without alignments)
83.540 Million cell updates/sec

Title: US-10-627-685a-26

Perfect score: 161

Sequence: 1 CRXNQKCFQHLDDCCSKCNKFNKCV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161	100.0	27	2	AAW35723 Kappa-con
2	161	100.0	27	4	AAU10218 Snail Kap
3	161	100.0	27	6	AAE38358 Conus pur
4	158	98.1	27	4	AAU10212 Snail Kap
5	158	98.1	27	4	AAU10206 Snail Kap
6	158	98.1	27	4	AAU10203 Snail Kap
7	158	98.1	27	6	AAE38352 Conus pur
8	158	98.1	27	6	AAE38346 Conus pur
9	158	98.1	27	6	AAE38343 Conus pur
10	157	97.5	27	4	AAU10207 Snail Kap
11	157	97.5	27	4	AAU10217 Snail Kap
12	157	97.5	27	6	AAE38357 Conus pur
13	157	97.5	27	6	AAE38347 Conus pur
14	156	96.9	27	4	AAU10214 Snail Kap
15	156	96.9	27	4	AAU10198 Snail Kap
16	156	96.9	27	6	AAE38338 Conus pur
17	156	96.9	27	6	AAE38354 Conus pur
18	155	96.3	27	4	AAU10200 Snail Kap
19	155	96.3	27	4	AAU10216 Snail Kap
20	155	96.3	27	4	AAU10205 Snail Kap
21	155	96.3	27	4	AAU10199 Snail Kap
22	155	96.3	27	4	AAU10196 Snail Kap
23	155	96.3	27	4	AAU10202 Snail Kap
24	155	96.3	27	4	AAU10210 Snail Kap
25	155	96.3	27	4	AAU10197 Snail Kap

AAU10204	Snail Kap	26	155	96.3	27	4	AAU10204
AAE38342	Conus pur	27	155	96.3	27	6	AAE38342
AAE38344	Conus pur	28	155	96.3	27	6	AAE38344
AAE38336	Conus pur	29	155	96.3	27	6	AAE38336
AAE38339	Conus pur	30	155	96.3	27	6	AAE38339
AAE38345	Conus pur	31	155	96.3	27	6	AAE38345
AAE38337	Conus pur	32	155	96.3	27	6	AAE38337
AAE38340	Conus pur	33	155	96.3	27	6	AAE38340
AAE38356	Conus pur	34	155	96.3	27	6	AAE38356
AAE38350	Conus pur	35	155	96.3	27	6	AAE38350
AAU10213	Snail Kap	36	153	95.0	27	4	AAU10213
AAU10209	Snail Kap	37	153	95.0	27	4	AAU10209
AAU10219	Snail Kap	38	153	95.0	27	4	AAU10219
AAU10201	Snail Kap	39	153	95.0	27	4	AAU10201
AAU10215	Snail Kap	40	153	95.0	27	4	AAU10215
AAU10211	Snail Kap	41	153	95.0	27	4	AAU10211
AAE38353	Conus pur	42	153	95.0	27	6	AAE38353
AAE38351	Conus pur	43	153	95.0	27	6	AAE38351
AAE38341	Conus pur	44	153	95.0	27	6	AAE38341
AAE38355	Conus pur	45	153	95.0	27	6	AAE38355
AAE38349	Conus pur	46	153	95.0	27	6	AAE38349
AAE38359	Conus pur	47	153	95.0	27	6	AAE38359
AAU10208	Snail Kap	48	151	93.8	27	4	AAU10208
AAE38348	Conus pur	49	151	93.8	27	6	AAE38348
AB966846	Omega-con	50	78.5	48.8	27	5	AB966846
AB966638	Omega-con	51	78.5	48.8	27	5	AB966638
AAE39628	SNX-202	52	75	46.6	26	2	AAE39628
AAE37774	SNX-202	53	75	46.6	26	2	AAE37774
AAU19570	SNX-202	54	75	46.6	26	2	AAU19570
AAW12985	Omega-con	55	75	46.6	26	2	AAW12985
AAW72625	Conus gen	56	75	46.6	26	2	AAW72625
AAW95584	Analog om	57	75	46.6	26	2	AAW95584
AAV56496	Analogue	58	75	46.6	26	3	AAV56496
AAU14370	Omega-con	59	75	46.6	26	3	AAU14370
AAU19462	Sequence	60	75	46.6	26	4	AAU19462
AB966887	Omega-con	61	74	46.0	26	5	AB966887
AB966679	Omega-con	62	74	46.0	30	5	AB966679
AB966666	Omega-con	63	73	45.3	72	5	AB966666
AAE39615	SVIB/SNX1	64	71	44.1	26	2	AAE39615
AAE37760	SVIB/SNX-1	65	71	44.1	26	2	AAE37760
AAU19551	Natural o	66	71	44.1	26	2	AAU19551
AAU12974	Omega-con	67	71	44.1	26	2	AAU12974
AAW72612	Conus gen	68	71	44.1	26	2	AAW72612
AAW95571	Omega-con	69	71	44.1	26	2	AAW95571
AAV56480	Natural o	70	71	44.1	26	3	AAV56480
AAU14359	Omega-con	71	71	44.1	26	3	AAU14359
AAE92221	Toxin pep	72	71	44.1	26	4	AAE92221
AAU19449	Primary s	73	71	44.1	26	4	AAU19449
AAU15126	Cone snail	74	71	44.1	26	5	AAU15126
AB966876	Omega-con	75	71	44.1	27	5	AB966876
AB966668	Omega-con	76	71	44.1	72	5	AB966668
AB966786	Omega-con	77	67	41.6	26	5	AB966786
AB96790	Omega-con	78	64	39.8	26	5	AB96790
AB96772	Omega-con	79	64	39.8	27	5	AB96772
AB96874	Omega-con	80	64	39.8	27	5	AB96874
AB96842	Omega-con	81	63.5	39.4	27	5	AB96842
AB966626	Omega-con	82	63.5	39.4	73	5	AB966626
AAW06589	Tyrosinas	83	63	39.1	38	2	AAW06589
AB98797	Conus bet	84	62.5	38.8	36	5	AB98797
AB98659	Conus bet	85	62.5	38.8	36	5	AB98659
AB96774	Omega-con	86	62	38.5	27	5	AB96774
AAU05927	Cone snail	87	62	38.5	76	4	AAU05927
AB96741	Omega-con	88	61.5	38.2	27	5	AB96741
AAU39616	MVIC/SNX	89	61	37.9	26	2	AAU39616
AAU39617	MVIC/SNX	90	61	37.9	26	2	AAU39617
AAU37762	MVIC/SNX	91	61	37.9	26	2	AAU37762
AAU19552	Natural o	92	61	37.9	26	2	AAU19552
AAU10205	Conus gen	93	61	37.9	26	2	AAU10205
AAU10199	Conus gen	94	61	37.9	26	2	AAU10199
AAU10196	Conus gen	95	61	37.9	26	2	AAU10196
AAU10202	Conus gen	96	61	37.9	26	2	AAU10202
AAU10210	Conus gen	97	61	37.9	26	2	AAU10210
AAU10197	Conus gen	98	61	37.9	26	3	AAU10197

99 . 61 37.9 26 3 AAY43715 Aay43715 Amino aci
100 61 37.9 26 3 AAB14377 Aab14377 Omega-con

ALIGNMENTS

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RESULT 1
AAW35723
ID AAW35723 standard; peptide; 27 AA.
XX
AC AAW35723;
XX
DT 03-APR-1998 (first entry)
XX
DE Kappa-conotoxin PVIIA.
XX
KW Kappa-conotoxin PVIIA; potassium channel; neurotransmitter release;
KW cone snail; venom; goldfish; delta-conotoxin PVIIA; disulphide.
XX
OS Conus purpurascens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..16
FT /note= "disulphide bond"
FT Modified-site 4
FT /note= "Optionally 4-trans-hydroxyproline, hydroxyproline
FT or proline"
FT Disulfide-bond 8..20
FT /note= "disulphide bond"
FT Disulfide-bond 15..26
FT /note= "disulphide bond"
XX
PN W09734925-A1.
XX
PD 25-SEP-1997.
XX
PF 14-MAR-1997; 9TWO-US003483.
XX
PR 18-MAR-1996; 96US-00619936.
XX
PA (UTAH ) UNIV UTAH RES FOUND.
XX
PI Terlau H, Shon K, Grilley MM, Olivera BM;
XX WPI; 1997-480162/44.
XX
PT New kappa-conotoxin peptides - which target potassium channels and can be
XX used to augment neurotransmitter release in e.g. autoimmune diseases.
XX
PS Claim 1; Page 23; 29pp; English.
XX
CC The present sequence represents a new kappa-conotoxin PVIIA which targets
XX potassium channels and can be used to augment neurotransmitter release in
XX pathological situations such as autoimmune diseases, e.g. Alzheimer's
XX disease, Lambert-Raton syndrome or myasthenia gravis. This peptide
XX together with delta-conotoxin PVIIA act synergistically to rapidly
XX immobilize fish which are injected with the two peptides. Injection of
XX kappa-conotoxin PVIIA alone results in different symptoms with an
XX injected fish becoming hyperactive and then contracting and suddenly
XX extending all major fins. This "fin-popping" occurs repeatedly resulting
XX in a series of jerky movements, but injection of only kappa-conotoxin
XX PVIIA does not immobilize or kill the fish
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 161; DB 2; Length 27;
Best Local Similarity 96.3%; Pred. No. 1e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRXNQKCFQHLDDCCSRKCNFNKCV 27
DB 1 CRIPNQKCFQHLDDCCSRKCNFNKCV 27

```

```

RESULT 2
AAU10218
ID AAU10218 standard; peptide; 27 AA.
XX
AC AAU10218;
XX
DT 16-JAN-2002 (first entry)
XX
DE Snail Kappa-conotoxin PVIIA analogue O4A.
XX
KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; O4A.
XX
OS Conus purpurascens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 4
FT /note= "Hydroxyproline"
FT Modified-site 27
FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX
PN W0200121648-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 200OWO-US025827.
XX
PR 22-SEP-1999; 99US-0155135P.
XX
PR 20-JUL-2000; 2000US-0219438P.
XX
PA (COGN-) COGNETIX INC.
XX
PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
XX Jones RR;
XX WPI; 2001-648090/74.
XX
PT Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
PS Claim 1; Page 28; 46pp; English.
XX
CC The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
SQ Sequence 27 AA;
Query Match 100.0%; Score 161; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 1e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRXNQKCFQHLDDCCSRKCNFNKCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNFNKCV 27

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RESULT 3
AAE38358
ID AAE38358 standard; peptide; 27 AA.

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XX AC AAE38358;
 XX XX 20-NOV-2003 (first entry)
 XX XX Conus purpurascens kappa-PVIIA analogue peptide, Q4A.
 XX XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX XX Conus purpurascens.
 OS XX WO2003063782-A2.
 XX XX 07-AUG-2003.
 XX XX 28-JAN-2003; 2003WO-US002384.
 PF XX 29-JAN-2002; 2002US-0352219P.
 XX XX (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI PI Olivera BM;
 PI PI WPI; 2003-679464/64.
 DR XX Protection and preservation of an organ e.g. heart of a mammal comprises
 XX PT use of a compound binding to kappa-PVIIA-binding site.
 XX PT Disclosure; Page 8; 32pp; English.
 PS XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX SQ Sequence 27 AA;
 Query Match 100.0%; Score 161; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 1e-10; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 DB 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 RESULT 4
 AAU10212
 ID AAU10212 standard; peptide; 27 AA.
 XX AC AAU10212;
 XX DT 16-JAN-2002 (first entry)
 XX XX Snail Kappa-conotoxin PVIIA analogue S17A.
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;

KW cerebral ischaemia; ocular ischaemia; asthma; S17A.
 XX Conus purpurascens.
 OS Synthetic.
 XX PH Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX XX WO200121648-A1.
 PN XX 29-MAR-2001.
 XX PD 21-SEP-2000; 2000WO-US025827.
 XX PF 22-SEP-1999; 99US-0155135P.
 XX PR 20-JUL-2000; 2000US-0219438P.
 XX XX (COGN-) COGNETIX INC.
 XX XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI PI Jones RR;
 PI WPI; 2001-648090/74.
 DR XX Treating disorders associated with radical depolarization of excitable
 XX PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 XX PT activating a KATP channel by administering to an individual a kappa-
 XX PT conotoxin PVIIA peptide.
 XX PS Claim 1; Page 28; 46pp; English.
 XX CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX SQ Sequence 27 AA;
 Query Match 98.1%; Score 158; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 2.2e-10; Indels 0; Gaps 0;
 Matches 26; Conservative 1; Mismatches 0;
 QY 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 DB 1 CRXNQKCFQHLDDCCSRKCNRFKCV 27
 RESULT 5
 AAU10206
 ID AAU10206 standard; peptide; 27 AA.
 XX AC AAU10206;
 XX DT 16-JAN-2002 (first entry)
 XX XX Snail Kappa-conotoxin PVIIA analogue F9Y.
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; F9Y.
 XX Conus purpurascens.
 OS Synthetic.
 XX

XX
PT Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX
PS Disclosure; Page 7; 32pp; English.
XX
CC The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, hypertension, angina, cerebral
CC peripheral circulation disturbances, haemorrhage, anxiety disorder,
CC vasospasm accompanying subarachnoid haemorrhage, cerebral ischaemia,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
CC peptide
XX
SQ Sequence 27 AA;

Query Match 98.1%; Score 158; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 2.2e-10;
Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CKIPNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 10

AAU10207

ID AAU10207 standard; peptide; 27 AA.

AC AAU10207;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue E2Q.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R2Q.
XX
OS Conus purpurascens.
XX Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"

XX WO200121648-A1.

PN 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

PR 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable

PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises

XX

PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
PS Claim 1; Page 28; 46pp; English.

XX The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
CC analogue of the invention
XX
SQ Sequence 27 AA;

Query Match 97.5%; Score 157; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 2.8e-10;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CQIXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 11

AAU10217

ID AAU10217 standard; peptide; 27 AA.

AC AAU10217;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue V27A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; V27A.
XX
OS Conus purpurascens.
XX Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27

FT /note= "The C-terminus is either a carboxyl group or an
FT amide group"

XX WO200121648-A1.

PN 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

PR 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

PI Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable

PT membrane e.g. cardiac, cerebral and ocular ischaemia and asthma comprises

XX activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
PS Claim 1; Page 28; 46pp; English.

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 157; DB 4; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||
 DB 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||

RESULT 12
 AAE38357
 ID AAE38357 standard; peptide; 27 AA.
 XX AC AAE38357;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, V27A.
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PN 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PS Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,

CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;

Query Match 97.5%; Score 157; DB 6; Length 27;
 Best Local Similarity 96.2%; Pred. No. 2.8e-10;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 |||||
 DB 1 CRIPNOKCFQHLDDCCSRKCNRFNKC 26
 |||||

RESULT 13
 AAE38347
 ID AAE38347 standard; peptide; 27 AA.
 XX AC AAE38347;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, R2Q.
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PN 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PS Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

Query Match 96.9%; Score 156; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 3.6e-10;
Matches 26; Conservative 0; Mismatched 1; Indel 1

RESULT 16
AAE38338
ID AAE38338 standard; peptide; 27 AA.
XX AC AAE38338;
XX AC AAE38338;
XX DT 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, I3A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Modified-site 4 /label= Hyp
FT FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 6; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRAPNOKCFQHLDDCCSRKCNRFNKCVCV 27
RESULT 17
AAE38354
ID AAE38354 standard; peptide; 27 AA.
XX AC AAE38354;
XX DT 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, L12A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Modified-site 4 /label= Hyp
FT FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRIPNOKCFQHADCCSRKCNRFNKCVCV 27
RESULT 18
AAU10200
ID AAU10200 standard; peptide; 27 AA.
XX AC AAU10200;
XX AC AAU10200;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R2A.

AC AAE38354;
XX 20-NOV-2003 (first entry)
XX DE Conus purpurascens kappa-PVIIA analogue peptide, L12A.
XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
XX KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
XX KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
XX KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
XX KW congestive heart failure; neuropathy; nephropathy; CABG.
XX OS Conus purpurascens.
XX FH Key Location/Qualifiers
FT Modified-site 4 /label= Hyp
FT FT
XX PN WO2003063782-A2.
XX PD 07-AUG-2003.
XX PF 28-JAN-2003; 2003WO-US002384.
XX PR 29-JAN-2002; 2002US-0352219P.
XX PA (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX DR WPI; 2003-679464/64.
XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX PS Disclosure; Page 8; 32pp; English.
XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasoospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
XX SQ Sequence 27 AA;
Query Match 96.9%; Score 156; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 3.6e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRXNOKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRIPNOKCFQHADCCSRKCNRFNKCVCV 27
RESULT 18
AAU10200
ID AAU10200 standard; peptide; 27 AA.
XX AC AAU10200;
XX AC AAU10200;
XX DT 16-JAN-2002 (first entry)
XX DE Snail Kappa-conotoxin PVIIA analogue R2A.

XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; RZA.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX WO200121648-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 XX
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 XX WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 27; 46pp; English.
 XX
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 XX Sequence 27 AA;
 XX
 XX Query Match 96.3%; Score 155; DB 4; Length 27;
 XX Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CAIXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 XX RESULT 19
 XX AAU10216
 ID AAU10216 standard; peptide; 27 AA.
 XX
 XX AAU10216;
 XX
 XX 16-JAN-2002 (first entry)
 XX
 XX Snail Kappa-conotoxin PVIIA analogue Q10A.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; Q10A.
 XX

OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX WO200121648-A1.
 XX
 XX 29-MAR-2001.
 XX
 XX 21-SEP-2000; 2000WO-US025827.
 XX
 XX 22-SEP-1999; 99US-0155135P.
 PR 20-JUL-2000; 2000US-0219438P.
 XX
 XX (COGN-) COGNETIX INC.
 XX
 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
 PI Jones RR;
 XX
 XX WPI; 2001-648090/74.
 XX
 XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.
 XX
 XX Claim 1; Page 28; 46pp; English.
 XX
 XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 XX Sequence 27 AA;
 XX
 XX Query Match 96.3%; Score 155; DB 4; Length 27;
 XX Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 XX Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 XX RESULT 20
 XX AAU10205
 ID AAU10205 standard; peptide; 27 AA.
 XX
 XX AAU10205;
 XX
 XX 16-JAN-2002 (first entry)
 XX
 XX Snail Kappa-conotoxin PVIIA analogue F9M.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; F9M.
 XX
 XX Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 4

FT Modified-site 27 /note= "Hydroxyproline"
 FT /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 XX
 PN WO200121648-A1.
 XX
 PD 29-MAR-2001.
 FT
 XX
 PF 21-SEP-2000; 2000WO-US025827.
 XX
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 PR 22-SEP-1999; 99US-0155135P.
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 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 21
 AAU10199
 ID AAU10199 standard; peptide; 27 AA.
 XX
 AC AAU10199;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 DE Snail Kappa-conotoxin PVIIA analogue K19A.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; K19A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27
 FT Modified-site /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX

PN WO200121648-A1.
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 PD 29-MAR-2001.
 XX
 PF 21-SEP-2000; 2000WO-US025827.
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 PR 22-SEP-1999; 99US-0155135P.
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 XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
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 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 4.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 22
 AAU10196
 ID AAU10196 standard; peptide; 27 AA.
 XX
 AC AAU10196;
 XX
 XX 16-JAN-2002 (first entry)
 DT
 DE Snail Kappa-conotoxin PVIIA analogue R18A.
 XX
 XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; R18A.
 XX
 OS Conus purpurascens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /note= "Hydroxyproline"
 FT Modified-site 27
 FT Modified-site /note= "The C-terminus is either a carboxyl group or an
 FT amide group"
 FT
 XX
 PN WO200121648-A1.
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 PD 29-MAR-2001.
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 XX 21-SEP-2000; 2000WO-US025827.

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CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 96.3%; Score 155; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
RESULT 25
AAU10197
ID AAU10197 standard; peptide; 27 AA.
AC AAU10197;
XX 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue R22A.
DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; R22A.
XX Conus purpurascens.
OS Synthetic.
OS Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
PN 29-MAR-2001.
XX 21-SEP-2000; 2000WO-US025827.
XX 22-SEP-1999; 99US-0155135P.
PR 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX WPI; 2001-648090/74.
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PT conotoxin PVIIA peptide.

XX Claim 1; Page 27; 46pp; English.
PS The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel
CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
CC PVIIA) peptide or its analogue, derivative or physiologically active
CC salt. The conotoxins are used for treating disorders associated with
CC radical depolarisation of excitable membrane by activating a KATP
CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
SQ Sequence 27 AA;
Query Match 96.3%; Score 155; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
DB 1 CRXNKKCFQHLDDCCSRKCNRFKCV 27
RESULT 26
AAU10204
ID AAU10204 standard; peptide; 27 AA.
AC AAU10204;
XX 16-JAN-2002 (first entry)
XX Snail Kappa-conotoxin PVIIA analogue K7A.
DE Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
KW cerebral ischaemia; ocular ischaemia; asthma; K7A.
XX Conus purpurascens.
OS Synthetic.
OS Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
XX WO200121648-A1.
PN 29-MAR-2001.
XX 21-SEP-2000; 2000WO-US025827.
XX 22-SEP-1999; 99US-0155135P.
PR 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX WPI; 2001-648090/74.
XX Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX Claim 1; Page 28; 46pp; English.
PS The invention relates to treating disorders associated with radical
CC depolarisation of excitable membrane by activating a KATP channel

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRIPNACFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 29
AAE38336
ID AAE38336 standard; peptide; 27 AA.
XX AAE38336;
AC AAE38336;
DT 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, R18A.
DE
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.
XX Conus purpurascens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT
FT
PN WO2003063782-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002384.
XX
XX 29-JAN-2002; 2002US-0352219P.
XX
XX (COGN-) COGNETIX INC.
PA (UTAH) UNIV UTAH RES FOUND.
XX
XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
XX
XX WPI; 2003-679464/64.
XX
XX Protection and preservation of an organ e.g. heart of a mammal comprises
PT use of a compound binding to kappa-PVIIA-binding site.
XX
XX Disclosure; Page 6; 32pp; English.
XX
XX The invention relates to kappa-PVIIA-related conotoxins and their use as
CC organ protectants. The invention also relates to a method of arresting,
CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
CC related conotoxins. The conotoxins can also be used for arresting,
CC protecting or preserving somatic cells. The invention is for the
CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
SQ Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRIPNACFQHLDDCCSRKCNRFNKCVCV 27
|||||

Db 1 CRIPNQCFOHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 30
AAE38339
ID AAE38339 standard; peptide; 27 AA.
XX AAE38339;
AC AAE38339;
DT 20-NOV-2003 (first entry)
XX Conus purpurascens kappa-PVIIA analogue peptide, K19A.
DE
XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
KW congestive heart failure; neuropathy; nephropathy; CABG.
XX Conus purpurascens.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 4 /label= Hyp
FT
FT
PN WO2003063782-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-US002384.
XX
XX 29-JAN-2002; 2002US-0352219P.
XX
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XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
PI Olivera BM;
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XX WPI; 2003-679464/64.
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CC peripheral circulation disturbances, hypertension, angina, cerebral
CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
CC ischaemic heart disease, asthma and congestive heart failure. The present
CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX peptide
SQ Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;
Best Local Similarity 92.6%; Pred. No. 4.7e-10;
Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

DB 1 CRIPNQCFOHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 31

AAE38345
 ID AAE38345 standard; peptide; 27 AA.
 XX
 AC AAE38345;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, F9M.
 KW
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT
 FN WO2003063782-A2.
 XX
 XX 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US002384.
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 PR
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 PA (UTAH) UNIV UTAH RES FOUND.
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 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 PI
 DR WPI; 2003-679464/64.
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 PT
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 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 4.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNQCQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 32
 AAE38337
 ID AAE38337 standard; peptide; 27 AA.
 XX
 AC AAE38337;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, R2A.
 KW
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;

DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, R22A.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX
 OS Conus purpurascens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT
 FN WO2003063782-A2.
 XX
 XX 07-AUG-2003.
 XX
 XX 28-JAN-2003; 2003WO-US002384.
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 PR
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 XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 PI
 DR WPI; 2003-679464/64.
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 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide
 XX
 SQ Sequence 27 AA;
 XX
 Query Match 96.3%; Score 155; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 4.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRINQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNQCQHLDDCCSRKCNRFNKCVCV 27
 XX
 RESULT 33
 AAE38340
 ID AAE38340 standard; peptide; 27 AA.
 XX
 AC AAE38340;
 XX
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Conus purpurascens kappa-PVIIA analogue peptide, R2A.
 XX
 KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;

KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

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XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

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 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
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 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;

Best Local Similarity 92.6%; Pred. No. 4.7e-10;

Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

DB 1 CAIPNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 34

AAE38356

ID AAE38356 standard; peptide; 27 AA.

XX AAE38356;

XX 20-NOV-2003 (first entry)

XX Conus purpurascens kappa-PVIIA analogue peptide, Q10A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

XX WO2003063782-A2.

XX 07-AUG-2003.

XX 28-JAN-2003; 2003WO-US002384.

XX 29-JAN-2002; 2002US-0352219P.

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XX (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

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 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 96.3%; Score 155; DB 6; Length 27;

Best Local Similarity 92.6%; Pred. No. 4.7e-10;

Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

DB 1 CRIPNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 35

AAE38350

ID AAE38350 standard; peptide; 27 AA.

XX AAE38350;

XX 20-NOV-2003 (first entry)

XX Conus purpurascens kappa-PVIIA analogue peptide, Q6A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

OS Conus purpurascens.

XX Key Location/Qualifiers

FH Modified-site 4 /label= Hyp

FT

XX	WO2003063782-A2.
XX	07-AUG-2003.
XX	28-JAN-2003; 2003WO-US002384.
XX	29-JAN-2002; 2002US-0352219P.
XX	(COGN-) COGNETIX INC.
XX	(UTAH) UNIV UTAH RES FOUND.
XX	Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
XX	Olivera BM;
XX	WPI; 2003-679464/64.
XX	Protection and preservation of an organ e.g. heart of a mammal comprises
XX	use of a compound binding to kappa-PVIIA-binding site.
XX	Disclosure; Page 7; 32pp; English.
XX	The invention relates to kappa-PVIIA-related conotoxins and their use as
XX	organ protectants. The invention also relates to a method of arresting,
XX	protecting and/or preserving an organ of a mammal using kappa-PVIIA-
XX	related conotoxins. The conotoxins can also be used for arresting,
XX	protecting or preserving somatic cells. The invention is for the
XX	treatment of arrhythmia, urinary incontinence, reperfusion injury,
XX	diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
XX	peripheral circulation disturbances, hypertension, angina, cerebral
XX	vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
XX	cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
XX	ischemic heart disease, asthma and congestive heart failure. The present
XX	sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
XX	peptide
XX	Sequence 27 AA;
XX	Query Match 96.3%; Score 155; DB 6; Length 27;
XX	Best Local Similarity 92.6%; Pred. No. 4.7e-10;
XX	Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	1 CR1XNOKCFQHLDDCCSRKCNFNKCV 27
Db	1 CR1PNAKCFQHLDDCCSRKCNFNKCV 27
RESULT 36	
AAU10213	
ID	AAU10213 standard; peptide; 27 AA.
XX	
AC	AAU10213;
XX	
DT	16-JAN-2002 (first entry)
XX	
DE	Snail Kappa-conotoxin PVIIA analogue N24A.
XX	
KW	Purple cone snail; Kappa-conotoxin PVIIA analogue; circulatory;
KW	cardioactive; antiaerthmatic; KATP channel activation; cardiac ischaemia;
KW	cerebral ischaemia; ocular ischaemia; asthma; N24A.
OS	Conus purpurascens.
XX	Synthetic.
XX	
Key	Location/Qualifiers
FT	Modified-site 4
FT	/note= "Hydroxyproline"
FT	Modified-site 27
FT	/note= "The C-terminus is either a carboxyl group or an
FT	amide group"
XX	
XX	WO200121648-A1.
XX	

PR 20-JUL-2000; 2000US-0219438P.
XX (COGN-) COGNETIX INC.
XX
XX
PI Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX
PT Treating disorders associated with radical depolarization of excitable
PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
PT activating a KATP channel by administering to an individual a kappa-
PT conotoxin PVIIA peptide.
XX
XX Claim 1; Page 28; 46pp; English.
XX
XX The invention relates to treating disorders associated with radical
XX depolarisation of excitable membrane by activating a KATP channel
XX comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
XX PVIIA) peptide or its analogue, derivative or physiologically active
XX salt. The conotoxins are used for treating disorders associated with
XX radical depolarisation of excitable membrane by activating a KATP
XX channel, especially cardiac ischaemia, cerebral ischaemia, ocular
XX ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
XX analogue of the invention
XX Sequence 27 AA;
SQ

Query Match 95.0%; Score 153; DB 4; Length 27;
Best Local Similarity 96.3%; Pred. No. 7.7e-10;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 38
AAU10219
ID AAU10219 standard; peptide; 27 AA.
XX
XX AAU10219;
AC
XX
XX 16-JAN-2002 (first entry)
DT
DE
DE Snail Kappa-conotoxin PVIIA analogue NSA.
XX
XX Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
XX cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
XX cerebral ischaemia; ocular ischaemia; asthma; NSA.
XX
XX Conus purpurascens.
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 4 /note= "Hydroxyproline"
FT Modified-site 27
FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
FT amide group"
FT
XX
XX WO200121648-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 21-SEP-2000; 2000WO-US025827.
PF
XX
XX 22-SEP-1999; 99US-0155135P.
PR
XX
XX 20-JUL-2000; 2000US-0219438P.
XX
XX (COGN-) COGNETIX INC.
PA
XX
XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI Jones RR;
XX
XX WPI; 2001-648090/74.
XX
XX Treating disorders associated with radical depolarization of excitable

PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 27; 46pp; English.

XX The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNQKCAQHLDDCCSRKCNRFNKCVCV 27

RESULT 40

AAU10215
 ID AAU10215 standard; peptide; 27 AA.

XX AC AAU10215;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue D13A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; D13A.

OS Conus purpurascens.
 OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"

PN WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 28; 46pp; English.

XX

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active
 CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRXNQKCAQHLDDCCSRKCNRFNKCVCV 27

RESULT 41

AAU10211

ID AAU10211 standard; peptide; 27 AA.

XX AC AAU10211;

DT 16-JAN-2002 (first entry)

DE Snail Kappa-conotoxin PVIIA analogue N21A.

KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KATP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; N21A.

OS Conus purpurascens.

OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 4 /note= "Hydroxyproline"

FT Modified-site 27 /note= "The C-terminus is either a carboxyl group or an
 FT amide group"

PN WO200121648-A1.

XX 29-MAR-2001.

XX 21-SEP-2000; 2000WO-US025827.

XX 22-SEP-1999; 99US-0155135P.

XX 20-JUL-2000; 2000US-0219438P.

XX (COGN-) COGNETIX INC.

XX Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;

XX Jones RR;

XX WPI; 2001-648090/74.

XX Treating disorders associated with radical depolarization of excitable
 PT membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises
 PT activating a KATP channel by administering to an individual a kappa-
 XX conotoxin PVIIA peptide.

PS Claim 1; Page 28; 46pp; English.

CC The invention relates to treating disorders associated with radical
 CC depolarisation of excitable membrane by activating a KATP channel
 CC comprising administering to an individual a kappa-conotoxin PVIIA (kappa-
 CC PVIIA) peptide or its analogue, derivative or physiologically active

CC salt. The conotoxins are used for treating disorders associated with
 CC radical depolarisation of excitable membrane by activating a KATP
 CC channel, especially cardiac ischaemia, cerebral ischaemia, ocular
 CC ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA
 CC analogue of the invention

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 4; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27
 |||||
 DB 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 42

AAE38353
 ID AAE38353 standard; peptide; 27 AA.

XX AC AAE38353;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, N24A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

PN WO2003063782-A2.

XX 07-AUG-2003.

PF 28-JAN-2003; 2003WO-US002384.

PR 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX SQ

Sequence 27 AA;

Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

|||||
 DB 1 CRINXQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 43

AAE38351
 ID AAE38351 standard; peptide; 27 AA.

XX AC AAE38351;

DT 20-NOV-2003 (first entry)

DE Conus purpurascens kappa-PVIIA analogue peptide, N21A.

XX Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.

XX Conus purpurascens.

XX Key Location/Qualifiers
 FH Modified-site 4 /label= Hyp
 FT

PN WO2003063782-A2.

XX 07-AUG-2003.

PF 28-JAN-2003; 2003WO-US002384.

PR 29-JAN-2002; 2002US-0352219P.

XX (COGN-) COGNETIX INC.

PA (UTAH) UNIV UTAH RES FOUND.

XX Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;

XX WPI; 2003-679464/64.

XX Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.

XX Disclosure; Page 7; 32pp; English.

XX The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 CC peptide

XX Sequence 27 AA;

Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;

XX AC AAE38349;
 XX DT 20-NOV-2003 (first entry)
 XX DE Conus purpurascens kappa-PVIIA analogue peptide, D14A.
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT FT
 XX PN WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 47
 ID AAE38359
 XX AAE38359 standard; peptide; 27 AA.
 XX AC AAE38359;
 XX DT 20-NOV-2003 (first entry)
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT FT
 XX PN WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 7; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 92.6%; Pred. No. 7.7e-10;
 Matches 25; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIPNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 47
 ID AAE38359
 XX AAE38359 standard; peptide; 27 AA.
 XX AC AAE38359;
 XX DT 20-NOV-2003 (first entry)
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT FT
 XX PN WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 48
 ID AAU10208
 XX AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue H11A.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KARP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H11A.

DE XX Conus purpurascens kappa-PVIIA analogue peptide, NSA.
 XX KW Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence;
 KW ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes;
 KW organ protectant; arrhythmia; reperfusion injury; hypertension; angina;
 KW retinopathy; coronary artery bypass graft surgery; acute heart failure;
 KW congestive heart failure; neuropathy; nephropathy; CABG.
 XX OS Conus purpurascens.
 XX FH Key Location/Qualifiers
 FT Modified-site 4 /label= Hyp
 FT FT
 XX PN WO2003063782-A2.
 XX PD 07-AUG-2003.
 XX PF 28-JAN-2003; 2003WO-US002384.
 XX PR 29-JAN-2002; 2002US-0352219P.
 XX PA (COGN-) COGNETIX INC.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PI Pemberton-Goodman KE, Jones RM, Temple DL, McIntosh JM;
 PI Olivera BM;
 XX DR WPI; 2003-679464/64.
 XX PT Protection and preservation of an organ e.g. heart of a mammal comprises
 PT use of a compound binding to kappa-PVIIA-binding site.
 XX PS Disclosure; Page 8; 32pp; English.
 XX CC The invention relates to kappa-PVIIA-related conotoxins and their use as
 CC organ protectants. The invention also relates to a method of arresting,
 CC protecting and/or preserving an organ of a mammal using kappa-PVIIA-
 CC related conotoxins. The conotoxins can also be used for arresting,
 CC protecting or preserving somatic cells. The invention is for the
 CC treatment of arrhythmia, urinary incontinence, reperfusion injury,
 CC diabetes, retinopathy, neuropathy, nephropathy, acute heart failure,
 CC peripheral circulation disturbances, hypertension, angina, cerebral
 CC vasospasm accompanying subarachnoid haemorrhage, anxiety disorder,
 CC cerebral ischaemia, coronary artery bypass graft (CABG) surgery,
 CC ischaemic heart disease, asthma and congestive heart failure. The present
 CC sequence is Conus purpurascens (purple cone snail) kappa PVIIA analogue
 XX peptide
 XX SQ Sequence 27 AA;
 Query Match 95.0%; Score 153; DB 6; Length 27;
 Best Local Similarity 96.3%; Pred. No. 7.7e-10;
 Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 DB 1 CRIXNKCQFQHLDDCCSRKCNRFNKCVCV 27
 RESULT 48
 ID AAU10208
 XX AAU10208 standard; peptide; 27 AA.
 XX AC AAU10208;
 XX DT 16-JAN-2002 (first entry)
 XX DE Snail Kappa-conotoxin PVIIA analogue H11A.
 XX KW Purple cone snail; kappa-conotoxin PVIIA analogue; circulatory;
 KW cardioactive; antiasthmatic; KARP channel activation; cardiac ischaemia;
 KW cerebral ischaemia; ocular ischaemia; asthma; H11A.

XX	Conus purpurascens.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 4
FT	/note= "Hydroxyproline"
FT	Modified-site 27
FT	/note= "The C-terminus is either a carboxyl group or an amide group"
FT	
XX	WO200121648-A1.
PN	
XX	29-MAR-2001.
XX	
PF	21-SEP-2000; 2000WO-US025827.
XX	
PR	22-SEP-1999; 99US-015513SP.
PR	20-JUL-2000; 2000US-0219438P.
XX	
PA	(COGN-) COGNETIX INC.
XX	
PI	Cornell-Bell AH, Pemberton KE, Temple DL, Layer RT, McCabe RT;
PI	Jones RR;
XX	
DR	WPI; 2001-648090/74.
XX	
PT	Treating disorders associated with radical depolarization of excitable membrane e.g. cardiac, cerebral and ocular ischemia and asthma comprises activating a KATP channel by administering to an individual a kappa-conotoxin PVIIA peptide.
PT	
XX	
PS	Claim 1; Page 28; 46pp; English.
XX	
CC	The invention relates to treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel comprising administering to an individual a kappa-conotoxin PVIIA (kappa-PVIIA) peptide or its analogue, derivative or physiologically active salt. The conotoxins are used for treating disorders associated with radical depolarisation of excitable membrane by activating a KATP channel, especially cardiac ischaemia, cerebral ischaemia, ocular ischaemia and asthma. The present sequence is a kappa-conotoxin PVIIA analogue of the invention
XX	
SQ	Sequence 27 AA;
	Query Match 93.8%; Score 151; DB 4; Length 27;
	Best Local Similarity 96.3%; Pred. No. 1.3e-09;
	Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Qy	1 CRXNOKCFQHLDCCSRKCNRFNCV 27
Dd	1 CRXNOKCFQALDDCCSRKCNRFNCV 27
RESULT 49	
AAE38348	
ID	AAE38348 standard; peptide; 27 AA.
AC	
XX	AAE38348;
XX	
DT	20-NOV-2003 (first entry)
DE	
XX	Conus purpurascens kappa-PVIIA analogue peptide, H1IA.
XX	
KW	Purple cone snail; kappa-PVIIA-related conotoxin; urinary incontinence; ischaemic heart disease; cerebral ischaemia; anxiety disorder; diabetes; organ protectant; arrhythmia; reperfusion injury; hypertension; angina; retinopathy; coronary artery bypass graft surgery; acute heart failure; congestive heart failure; neuropathy; nephropathy; CABG.
XX	
XX	Conus purpurascens.
XX	

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XX PD 31-JAN-2002.
XX XX
XX PD 23-JUL-2001; 2001WO-US023041.
XX XX
XX PF 21-JUL-2000; 2000US-0219616P.
XX PR 05-FEB-2001; 2001US-0265888P.
XX XX
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (COGN-) COGNETIX INC.
XX XX
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
XX PI Jacobsen R, Jones RM, Cartier GE;
XX DR WPI; 2002-257318/30.
XX XX
XX PT New omega-conopeptides useful for treating disorders associated with
XX PT voltage gated ion channels e.g. pain, inflammation, neurologic or
XX PT cardiovascular disorders.
XX PS Claim 1(a); Page 71; 195pp; English.
XX CC The invention relates to isolated omega-conopeptides, nucleic acid
XX CC sequences encoding them, and propeptide sequences. The activity of the
XX CC peptides of the invention may be described as, analgesic, anticonvulsant,
XX CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
XX CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
XX CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
XX CC by modulating the activity of voltage gated ion channels. They may be
XX CC used for treating or preventing disorders associated with voltage gated
XX CC ion channels such as neurological disorders, e.g. seizure (associated
XX CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
XX CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
XX CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
XX CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
XX CC They may also be used for treating psychiatric disorders e.g. psychosis,
XX CC anxiety or schizophrenia. The analgesic agents of the invention show
XX CC diminished side effects and toxicity, and are non-addictive. The
XX CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
XX CC toxin sequences
XX SQ Sequence 27 AA;

Query Match 48.8%; Score 78.5; DB 5; Length 27;
Best Local Similarity 46.2%; Pred. No. 0.098;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : ||| | ||| : |||
Db 2 CRPKGRKCFPHQKDCNKTCTR-SKC 26

RESULT 51
ABB96638
ID ABB96638 standard; peptide; 72 AA.
XX XX
XX AC ABB96638;
XX XX
XX DT 12-JUL-2002 (first entry)
XX XX
XX DE Omega-conopeptide E6.2 propeptide.
XX XX
XX KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
XX KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
XX KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
XX KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
XX KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
XX KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
XX KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
XX KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
XX KW psychosis; anxiety; schizophrenia.
XX OS Conus ermineus.

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XX WO200207675-A2.
XX 31-JAN-2002.
XX 23-JUL-2001; 2001WO-US023041.
XX 21-JUL-2000; 2000US-0219616P.
XX PR 05-FEB-2001; 2001US-0265888P.
XX XX
XX PA (UTAH ) UNIV UTAH RES FOUND.
XX PA (COGN-) COGNETIX INC.
XX XX
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
XX PI Jacobsen R, Jones RM, Cartier GE;
XX DR WPI; 2002-257318/30.
XX DR N-PSDB; ABL98897.
XX XX
XX PT New omega-conopeptides useful for treating disorders associated with
XX PT voltage gated ion channels e.g. pain, inflammation, neurologic or
XX PT cardiovascular disorders.
XX PS Claim 1(c); Page 42; 195pp; English.
XX XX
XX CC The invention relates to isolated omega-conopeptides, nucleic acid
XX CC sequences encoding them, and propeptide sequences. The activity of the
XX CC peptides of the invention may be described as, analgesic, anticonvulsant,
XX CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
XX CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary, act
XX CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
XX CC by modulating the activity of voltage gated ion channels. They may be
XX CC used for treating or preventing disorders associated with voltage gated
XX CC ion channels such as neurological disorders, e.g. seizure (associated
XX CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
XX CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
XX CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
XX CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
XX CC They may also be used for treating psychiatric disorders e.g. psychosis,
XX CC anxiety or schizophrenia. The analgesic agents of the invention show
XX CC diminished side effects and toxicity, and are non-addictive. The
XX CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
XX CC propeptide sequences
XX SQ Sequence 72 AA;

Query Match 48.8%; Score 78.5; DB 5; Length 72;
Best Local Similarity 46.2%; Pred. No. 0.22;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : ||| | ||| : |||
Db 47 CRPKGRKCFPHQKDCNKTCTR-SKC 71

RESULT 52
AAR39628
ID AAR39628 standard; peptide; 26 AA.
XX XX
XX AC AAR39628;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 20-DEC-1993 (first entry)
XX XX
XX DE SNX-202.
XX XX
XX KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
XX KW calcium channel; neuron; contraction; guinea pig; ileum; MVIIA;
XX KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
XX KW narcotics.
XX XX
XX OS Synthetic.
XX OS

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PH Key Location/Qualifiers
FT Disulfide-bond 1. .16
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
FT Modified-site 26
FT /note= "Amidated C-terminal"
XX
PN WO9313128-A1.
XX
XX 08-JUL-1993.
XX
XX 30-DEC-1992; 92WO-US011349.
XX
XX 30-DEC-1991; 91US-00814759.
XX
XX (NEUR-) NEUREX CORP.
XX
XX Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
PI WPI; 1993-227270/28.
DR
XX Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
PT pain etc.
XX
XX Claim 1; Fig 2; 90pp; English.
XX
XX The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
CC derivatives of these, which may be used to produce analgesia in a mammal.
CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
CC tissue. This is shown by the peptides ability to stimulate contraction in
CC guinea pig ileum and to bind to OCT MVIIR binding sites present in
CC neuronal tissue. OCTs are components of peptide toxins derived from
CC marine snails of the genus Conus, and act as calcium channel blockers.
CC These OCTs may be used to replace opioids in the treatment of chronic pain
CC or to reduce the opiod dosage required. This helps to reduce dependence
CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 26 AA;
SQ
Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
Db 1 CKLKGQSCSLMYDCCSGCGSGKC 26
RESULT 53
AAR37774
ID AAR37774 standard; peptide; 26 AA.
XX
XX AAR37774;
AC
XX
XX 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
XX SNX-202.
DE
XX
XX Ischaemia; neuronal; omega-conotoxin; OCT; MVIIR; MVIIC; MVIID; MVIIB;
KW GVIA; GVIIA; RVIA; SVIA; TVIA; SVIB; SNX-207; stroke; delayed treatment;
KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW N-channel mediated neurotransmitter release.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1. .16
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
XX

PN WO9310145-A1.
XX
XX 27-MAY-1993.
PD
XX
XX 12-NOV-1992; 92WO-US009766.
PF
XX
XX 12-NOV-1991; 91US-00789913.
PR 17-JUL-1992; 92US-00916478.
XX
XX (NEUR-) NEUREX CORP.
PA
XX
XX Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
PI Yamashiro DH;
FI WPI; 1993-182487/22.
XX
XX Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
PT bind specifically to omega-conotoxin MVIIR binding sites.
XX
XX Disclosure; Fig 2; 103pp; English.
XX
XX The C-terminal is amidated. Ischaemia-related neuronal damage in mammals
CC is reduced by admin. 4-24 hr after onset of ischaemia, of a cpd. (I)
CC which binds selectively to an omega-conotoxin (OCT) MVIIR site in
CC neuronal tissue. (I) has selectivity at least 100 expressed as ratio of
CC binding affinity for the MVIIR site to that for the MVIIC site. (I) is
CC one of the OCTs MVIIR, MVIIB, GVIA, GVIIA or RVIA or it is the cpd. SNX-
CC 207. (I) is esp. used to reduce neuronal damage caused by stroke. By
CC delaying admin. for some time (compare US05051403 where cpds. are given
CC within 1 hr of the onset of ischaemia) a greater redn. in neuronal damage
CC is achieved. (I) is admin. e.g. by intracerebroventricular (ICV)
CC injection at 0.1-20 microg/kg, but can also be given i.v. (opt. after
CC treatment with antihistamines to minimise redn. in blood pressure caused
CC by (I)). (I) is also at least as effective as the specified conotoxins
CC for (1) selective inhibition of N-type voltage-gated Ca currents in
CC neuronal tissue and (2) selective inhibition of N-channel mediated
CC neurotransmitter release in neuronal tissue. Primary sequences of omega-
CC conopeptides are given in AAR37752-62. Several analog omega-conopeptides
CC are given in AAR37763-76. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 26 AA;
SQ
Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
Db 1 CKLKGQSCSLMYDCCSGCGSGKC 26
RESULT 54
AAW19570
ID AAW19570 standard; peptide; 26 AA.
XX
XX AAW19570;
AC
XX
XX 14-OCT-1997 (first entry)
DT
XX
XX SNX-202, omega conopeptide derivative used for pain relief.
DE
XX
XX Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
KW N-type voltage-sensitive calcium channel; block; Conus.
KW
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 26
FT /note= "amidated"
XX
XX WO9701351-A1.
XX
XX 16-JAN-1997.
PD

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XX 26-JUN-1996; 96WO-US011041.
XX PF
XX 27-JUN-1995; 95US-00496947.
XX PR
XX 08-MAR-1996; 96US-00613400.
XX PR
XX (NEUR-) NEUREX CORP.
XX PA
XX Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
XX PI Gadbois T, Pettus MR, Luther RR;
XX PI
XX WPI; 1997-100012/09.
XX DR
XX Stable omega-conopeptide compositions - for producing analgesia and for
XX PT inhibiting progression of neuropathic pain disorders.
XX PT
XX PS Disclosure; Fig 4; 47pp; English.
XX PS
XX AAW19555-W19572 are omega conopeptides (OCs) derived from natural
XX CC peptides from Conus sp. (cone snails). The peptides and their analogues
XX CC are used as analgesics acting by blocking N-type voltage-sensitive
XX CC calcium channels. The OCs can be used to treat neuropathic pain as a
XX CC result of e.g. insult to the spinal cord or peripheral nerves, cancer,
XX CC bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes
XX CC zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
XX CC hyperalgesia. The OCs are preferably administered in a medicament via an
XX CC epidural route in a continuous infusion or sustained release formulation.
XX CC The OCs can provide pain relief when administered epidurally in the
XX CC absence of a permeation enhancer, at doses that are comparable to
XX CC effective analgesic doses using intrathecal administration. OC
XX CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
XX CC They also confer stability to solutions containing them for prolonged
XX CC treatment methods and long-term storage
XX CC
XX SQ Sequence 26 AA;

Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CLKLGQSCSRLMYDCCSGCGSGKC 26

RESULT 55
AAW12985
ID AAW12985 standard; peptide; 26 AA.
XX AC
XX AAW12985;
XX AC
XX 25-MAR-2003 (revised)
XX DT 22-APR-1997 (first entry)
XX DT
XX Omega conopeptide SNX-202.
XX DE
XX Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
XX KW neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
XX KW acute dystonic reactions; inflammation; epilepsy.
XX KW
XX Synthetic.
XX OS
XX US5587454-A.
XX PN
XX 24-DEC-1996.
XX PD
XX 15-APR-1993; 93US-00049794.
XX PF
XX 30-DEC-1991; 91US-00814759.
XX PR
XX 30-DEC-1992; 92WO-US011349.
XX PR
XX (NEUR-) NEUREX CORP.
XX PA
XX

PI Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
XX DR WPI; 1997-064830/06.
XX DR
XX Omega conopeptide(s) - useful as analgesics, esp. for treating
XX PT neuropathic pain.
XX PT
XX Disclosure; Col 51-52; 58pp; English.
XX PS
XX The present peptide is an omega conopeptide, useful as an analgesic,
XX CC especially for treating neuropathic pain. The peptide, which can be
XX CC prepared by solid phase synthesis, can also be used to inhibit neuronal
XX CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
XX CC reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
XX CC PF field.)
XX CC
XX SQ Sequence 26 AA;

Query Match 46.6%; Score 75; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
|:::|:::|:::|:::|:::|:::|
Db 1 CLKLGQSCSRLMYDCCSGCGSGKC 26

RESULT 56
AAW72625
ID AAW72625 standard; peptide; 26 AA.
XX AC
XX AAW72625;
XX AC
XX 27-AUG-2003 (revised)
XX DT 06-JAN-1999 (first entry)
XX DT
XX Conus genus analogue omega-conopeptide SNX-202.
XX DE
XX Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
XX KW nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
XX KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
XX KW rheumatoid arthritis; epilepsy.
XX KW
XX Conus.
XX OS
XX US5824645-A.
XX PN
XX 20-OCT-1998.
XX PD
XX 01-NOV-1996; 96US-00742774.
XX PF
XX 30-DEC-1991; 91US-00814759.
XX PR
XX 15-APR-1993; 93US-00049794.
XX PR
XX 03-JUL-1996; 96US-00675354.
XX PR
XX (NEUR-) NEUREX CORP.
XX PA
XX Miljanich GP, Valentino KL, Gohil KC, Justice A, Singh T;
XX PI
XX WPI; 1998-582596/49.
XX DR
XX Treatment of inflammation, comprises administration of omega-conopeptide
XX PT - effective to block voltage-gated calcium channels, bind with high
XX PT affinity to omega-conopeptide binding site, and inhibit neurotransmitter
XX PT release.
XX PT
XX Disclosure; Fig 2; 58pp; English.
XX PS
XX A method has been developed for the treatment of inflammation in a
XX CC subject. The method comprises administration of an omega-conopeptide
XX CC effective to: (i) block voltage-gated calcium channels; (ii) bind with
XX CC high affinity to an omega-conopeptide binding site; and (iii) inhibit
XX CC neurotransmitter release from nervous tissue. The method is used to treat

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Query Match 46.6%; Score 75; DB 4; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.23;
Matches 11: Conservative 5; Mismatches 10; Indels

Local Samirity	Indels	Gaps
Mismatches	5; Mismatches	10; Indels
Matches	11; Conservative	0; Gaps

QY 1 CRXNQKCFHLDCCSRKCNRFNC 26
 Db 1 CKLKGSCSLMYDCCSGCGRGKC 26

RESULT 61
 ABB96887
 ID ABB96887 standard; peptide; 26 AA.
 AC ABB96887;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide S6.2 toxin sequence.
 XX

KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus striatus.
 XX

PN WO200207675-A2.
 XX

PD 31-JAN-2002.
 XX

PF 23-JUL-2001; 2001WO-US023041.
 XX

PR 21-JUL-2000; 2000US-0219616P.
 XX

PR 05-FEB-2001; 2001US-0265888P.
 XX

PA (UTAH) UNIV UTAH RES FOUND.
 XX

PA (COGN-) COGNETIX INC.
 XX

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 XX

PI Jacobsen R, Jones RM, Cartier GE;
 XX

DR WPI; 2002-257318/30.
 XX

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX

PS Claim 1(a); Page 72; 195pp; English.
 XX

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences
 XX

XX Sequence 26 AA;
 SQ

Query Match 46.0%; Score 74; DB 5; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.29;
 Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNQKCFHLDCCSRKCNRFNC 26
 Db 1 CKLKGSCSLMYDCCSGCGRGKC 26

RESULT 62
 ABB96679
 ID ABB96679 standard; peptide; 30 AA.
 AC ABB96679;
 XX

DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide S6.2 propeptide.
 XX

KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus striatus.
 XX

PN WO200207675-A2.
 XX

PD 31-JAN-2002.
 XX

PF 23-JUL-2001; 2001WO-US023041.
 XX

PR 21-JUL-2000; 2000US-0219616P.
 XX

PR 05-FEB-2001; 2001US-0265888P.
 XX

PA (UTAH) UNIV UTAH RES FOUND.
 XX

PA (COGN-) COGNETIX INC.
 XX

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 XX

PI Jacobsen R, Jones RM, Cartier GE;
 XX

DR WPI; 2002-257318/30.
 XX

DR N-PSDB; ABL98938.
 XX

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX

PS Claim 1(c); Page 62; 195pp; English.
 XX

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
 CC propeptide sequences
 XX

Query Match	44.1%;	Score 71;	DB 2;	Length 26;
Best Local Similarity	42.3%;	Pred. No. 0.62;		

Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
 Db 1 CLKKGSCRTSYDCCSGCGRSKC 26

RESULT 65

AAAR37760
 ID AAR37760 standard; peptide; 26 AA.

AC AAR37760;

DT 25-MAR-2003 (revised)
 DT 08-SEP-1993 (first entry)

DE SVIB/SNX-183.

KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
 KW GVIA; GVIIA; RVIA; SVIA; SVIB; SNX-207; stroke; delayed treatment;
 KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
 KW N-channel mediated neurotransmitter release.

OS Synthetic.

FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26

PN WO9310145-A1.

PD 27-MAY-1993.

PF 12-NOV-1992; 92WO-US009766.

PR 12-NOV-1991; 91US-00789913.

PR 17-JUL-1992; 92US-00916478.

PA (NEUR-) NEUREX CORP.

PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
 PI Yamashiro DH;

DR WPI; 1993-182487/22.

PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
 bind specifically to omega-conotoxin MVIIA binding sites.

PS Disclosure; Fig 1; 103pp; English.

CC Ischaemia-related neuronal damage in mammals is reduced by admin., 4-24
 CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
 CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
 CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
 CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
 CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
 CC damage caused by stroke. By delaying admin. for some time (compare
 CC US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a
 CC greater redn. in neuronal damage is achieved. (I) is admin. e.g. by
 CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
 CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
 CC in blood pressure caused by (I)). (I) is also at least as effective as
 CC the specified conotoxins for (I). (I) is also at least as effective as
 CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
 CC channel mediated neurotransmitter release in neuronal tissue. Primary
 CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
 CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
 CC correct PN field.)

Sequence 26 AA;

Query Match 44.1%; Score 71; DB 2; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.62;
 Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
 Db 1 CLKKGSCRTSYDCCSGCGRSKC 26

RESULT 66

AAW19551
 ID AAW19551 standard; peptide; 26 AA.

AC AAW19551;

DT 27-AUG-2003 (revised)
 DT 13-OCT-1997 (first entry)

DE Natural omega-conopeptide SVIB/SNX-183 used for pain relief.

KW Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;

KW N-type voltage-sensitive calcium channel; block; Conus.

OS Conus.

FH Key Location/Qualifiers

FT Modified-site 26 /note= "optionally amidated"
 FT FT
 XX XX

PN WO9701351-A1.

PD 16-JAN-1997.

PF 26-JUN-1996; 96WO-US011041.

PR 27-JUN-1995; 95US-00496847.

PR 08-MAR-1996; 96US-00613400.

PA (NEUR-) NEUREX CORP.

PI Amstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
 PI Gadbois T, Pettus MR, Luther RR;

DR WPI; 1997-100012/09.

PT Stable omega conopeptide compositions - for producing analgesia and for
 inhibiting progression of neuropathic pain disorders.

PS Disclosure; Fig 2, Fig 3; 47pp; English.

CC AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated
 CC from Conus sp. (cone snails). The peptides and their analogues are used
 CC as analgesics acting by blocking N-type voltage-sensitive calcium
 CC channels. The OCs can be used to treat neuropathic pain as a result of
 CC e.g. insult to the spinal cord or peripheral nerves, cancer, bone
 CC degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster
 CC neuropathy, diabetic neuropathy, hyperesthesia, allodynia or
 CC hyperalgesia. The OCs are preferably administered in a medicament via an
 CC epidural route in a continuous infusion or sustained release formulation.
 CC The OCs can provide pain relief when administered epidurally in the
 CC absence of a permeation enhancer, at doses that are comparable to
 CC effective analgesic doses using intrathecal administration. OC
 CC formulations comprising an OC and a carboxylic acid buffer anti-oxidant.
 CC they also confer stability to solutions containing them for prolonged
 CC treatment methods and long-term storage. (Updated on 27-AUG-2003 to
 CC correct OS field.)

Sequence 26 AA;

Query Match 44.1%; Score 71; DB 2; Length 26;
 Best Local Similarity 42.3%; Pred. No. 0.62;

Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26

```
Db      1 CKLKGQSCRKTSYDCCSGCRSGKC 26
      |:::| | | | | | | | | | | |
RESULT 67
AAW12974
ID AAW12974 standard; peptide; 26 AA.
XX
XX AAW12974;
AC
XX 25-MAR-2003 (revised)
DT 22-APR-1997 (first entry)
XX
XX Omega conopeptide SNX-183.
DE
XX Omega conopeptide; analgesic; treatment; neuropathic pain; inhibition;
KW neuronal damage; schizophrenia; tardive dyskinesia; analgesia;
KW acute dystonic reactions; inflammation; epilepsy.
XX
OS Synthetic.
XX
XX US5587454-A.
PN
XX
XX 24-DEC-1996.
PD
XX
XX 15-APR-1993; 93US-00049794.
PF
XX
XX 30-DEC-1991; 91US-00814759.
PR
XX 30-DEC-1992; 92WO-US011349.
XX
XX (NEUR-) NEUREX CORP.
PA
XX
XX Gohil KC, Miljanich GP, Valentino KL, Justice A, Singh T;
PI WPI; 1997-064830/06.
DR
XX Omega conopeptide(s) - useful as analgesics, esp. for treating
PT neuropathic pain.
PT
XX
XX Disclosure; Col 45-46; 58pp; English.
PS
XX The present peptide is an omega conopeptide, useful as an analgesic,
CC especially for treating neuropathic pain. The peptide, which can be
CC prepared by solid phase synthesis, can also be used to inhibit neuronal
CC damage and treat schizophrenia, tardive dyskinesia, acute dystonic
CC reactions, inflammation and epilepsy. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
XX Sequence 26 AA;
SQ
      Query Match 44.1%; Score 71; DB 2; Length 26;
      Best Local Similarity 42.3%; Pred. No. 0.62;
      Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
   |:::| | | | | | | | | | | |
Db 1 CKLKGQSCRKTSYDCCSGCRSGKC 26

RESULT 68
AAW72612
ID AAW72612 standard; peptide; 26 AA.
XX
XX AAW72612;
AC
XX 27-AUG-2003 (revised)
DT 06-JAN-1999 (first entry)
XX
XX Conus genus natural omega-conopeptide SVIB/SNX-183.
DE
XX Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
KW nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;

KW rheumatoid arthritis; epilepsy.
XX
OS Conus.
XX
XX US5824645-A.
PN
XX
XX 20-OCT-1998.
PD
XX
XX 01-NOV-1996; 96US-00742774.
PF
XX
XX 30-DEC-1991; 91US-00814759.
PR
XX 15-APR-1993; 93US-00049794.
XX
XX 03-JUL-1996; 96US-00675354.
XX
XX (NEUR-) NEUREX CORP.
PA
XX
XX Miljanich GP, Valentino KL, Gohil KC, Justice A, Singh T;
PI WPI; 1998-582596/49.
DR
XX
XX Treatment of inflammation, comprises administration of omega-conopeptide
PT - effective to block voltage-gated calcium channels, bind with high
PT affinity to omega-conopeptide binding site, and inhibit neurotransmitter
PT release.
XX
XX Disclosure; Fig 1; 58pp; English.
PS
XX
XX A method has been developed for the treatment of inflammation in a
CC subject. The method comprises administration of an omega-conopeptide
CC effective to: (i) block voltage-gated calcium channels; (ii) bind with
CC high affinity to an omega-conopeptide binding site; and (iii) inhibit
CC neurotransmitter release from nervous tissue. The method is used to treat
CC inflammation and associated pain. The treatment can also be used to
CC produce analgesia (especially in subjects experiencing neuropathic pain);
CC and to treat schizophrenia, tardive dyskinesia and acute dystonic
CC reactions, rheumatoid arthritis, and epilepsy. The present sequence
CC represents a natural omega-conopeptide. Omega-conopeptides are components
CC of peptide toxins produced by marine snails of the genus Conus, and which
CC act as calcium channel blockers. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
XX Sequence 26 AA;
SQ
      Query Match 44.1%; Score 71; DB 2; Length 26;
      Best Local Similarity 42.3%; Pred. No. 0.62;
      Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
   |:::| | | | | | | | | | | |
Db 1 CKLKGQSCRKTSYDCCSGCRSGKC 26

RESULT 69
AAW95571
ID AAW95571 standard; protein; 26 AA.
XX
XX AAW95571;
AC
XX
XX 29-MAR-1999 (first entry)
DT
XX
XX Omega-conopeptide SVIB/SNX-183.
DE
XX
XX Omega-conopeptide; peptide toxin; snail; calcium channel blocker;
KW analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
XX
XX Synthetic.
OS
OS Conus sp.
XX
XX Key Location/Qualifiers
FT Modified-site 26 /note= "C-terminal amide"
XX
XX US5859186-A.
PN
```


DR WPI; 2000-490177/43.

XX Selecting a compound for producing analgesia involves measuring activity

PT of test compound in blocking voltage-gated calcium channels, binding to

PT omega conopeptide binding site and inhibiting norepinephrine release.

XX Example 4; Fig 1; 58pp; English.

XX The present sequence is an omega-conopeptide from marine snails of the

CC genus Conus. Omega-conopeptides are components of peptide toxins produced

CC by the cone snails, and which act as calcium channel blockers. Natural

CC omega-conopeptides and their derivatives may be useful for producing

CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega

CC -conopeptide binding sites, which are present mainly in neuronal tissue,

CC and inhibit norepinephrine release from nervous tissue. Conopeptides such

CC as MWIIA and TWIA are effective as therapeutic agents for treating

CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute

CC dystonic reactions, inflammation and epilepsy

XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 3; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.62;

Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26

Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 26

RESULT 72

AAB92221

ID AAB92221 standard; peptide; 26 AA.

XX

AC AAB92221;

XX

DT 22-JUN-2001 (first entry)

XX

DE Toxin peptide SEQ ID NO:1397.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;

KW blood component; modification; succinimidy; maleimido group; amino;

KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

FN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013576.

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX

XX WPI; 2001-112059/12.

DR

XX Modifying and attaching therapeutic peptides to albumin prevents

PT peptidase degradation, useful for increasing length of in vivo activity.

XX

PS Disclosure; Page 653-654; 733pp; English.

XX

XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a

CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to

CC a less therapeutically active amino acid region (IV), which covalently

CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth

CC factors and neurotransmitters, to protect them from peptidase activity in

CC vivo for the treatment of various disorders. Endogenous therapeutic

CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.

CC Modifying and attaching therapeutic peptides to albumin prevents or

CC reduces the action of peptidases to increase length of activity (half

CC life) and specificity as bonding to large molecules decreases

CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the

CC exemplification of the present invention

XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 4; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.62;

Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26

Db 1 CKLKGQSCRKTSYDCSGSGRSGKC 26

RESULT 73

AAB19449

ID AAB19449 standard; peptide; 26 AA.

XX

AC AAB19449;

XX

DT 06-MAR-2001 (first entry)

XX

DE Primary sequence of a natural omega-conopeptide SVIB/SNX-183.

XX

KW Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;

KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;

KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;

KW epilepsy.

XX

OS Conus sp.

XX

FF Key Location/Qualifiers

FT Disulfide-bond 1..15

FT Disulfide-bond 8..19

FT Disulfide-bond 15..26

FT Modified-site 26

FT /note= "amidated C-terminal"

XX

PN US6136786-A.

XX

PD 24-OCT-2000.

XX

PF 09-SEP-1999; 99US-00392979.

XX

PR 30-DEC-1991; 91US-00814759.

PR 15-APR-1993; 93US-00049794.

PR 23-JUN-1993; 93US-00081863.

PR 03-JUL-1996; 96US-00675354.

PR 01-NOV-1996; 96US-00742774.

PR 21-AUG-1998; 98US-00138439.

PR 23-APR-1999; 99US-00298017.

XX

PA (ELAN-) ELAN PHARM INC.

XX

PI Singh T, Gohl KC, Valentino KL, Miljanich GP, Justice A;

XX

XX WPI; 2001-030946/04.

DR

XX Enhancing analgesia produced by opiates by administering an omega-

PT conopeptide that inhibits electrically stimulated contraction of guinea

PT pig ileum and binds to omega-conopeptide MWIIA binding sites in neuronal

PT tissues.

XX

PS Disclosure; Fig 1; 58pp; English.

XX The present sequence represents an omega-conopeptide. Omega-conopeptides
CC are components of peptide toxins which act as voltage-gated calcium
CC channel inhibitors. The peptides are used to enhance the analgesic effect
CC produced by an opiate in a mammalian subject. The method comprises
CC administering to the subject an omega-conopeptide which is able to
CC inhibit electrically stimulated contraction of the guinea pig ileum and
CC bind to omega-conopeptide WIIIA binding sites present in neuronal tissue.
CC Omega-conopeptides are useful for enhancing the analgesic effect produced
CC by an opiate. Omega-conopeptides may also be used in the treatment of
CC pain, in reducing neuronal damage related to an ischemic condition in
CC mammals, and in treating schizophrenia, tardive dyskinesia and acute
CC dystonic reactions, inflammation and epilepsy
XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 4; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 25

DB 1 CLKKGQSCRKTSYDCCSGSGRSGKC 25

RESULT 74

AAO15126

ID AAO15126 standard; peptide; 26 AA.

AC AAO15126;

XX 22-AUG-2002 (first entry)

DE Cone snail w-conotoxin peptide SVIB.

KW Cone snail; venomous saliva; calcium channel blocking activity;
KW stenocardia; hypertension; myocarditis; arrhythmia; cerebral ischaemia;
KW w-conotoxin.

OS Conus sp.

XX JP2002080499-A.

XX 19-MAR-2002.

XX 01-SEP-2000; 2000JP-00266187.

XX 01-SEP-2000; 2000JP-00266187.

XX (SUNR) SUNTORY LTD.

XX WPI; 2002-421068/45.

XX A new peptide derived from venomous saliva of assassin bug, has calcium
XX channel blocking activity.

XX Disclosure; Page 4; 26pp; Japanese.

XX The invention comprises peptides having calcium channel blocking
XX activities which are derived from the venomous saliva of assassin bugs.
XX The calcium channel blocking peptides of the invention are useful for
XX treating stenocardia, hypertension, myocarditis, arrhythmia and cerebral
XX ischaemia. The present amino acid sequence represents a cone snail w-
XX conotoxin peptide
XX

SQ Sequence 26 AA;

Query Match 44.1%; Score 71; DB 5; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.62;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26

DB 1 CLKKGQSCRKTSYDCCSGSGRSGKC 26

RESULT 75

ABB96876

ID ABB96876 standard; peptide; 27 AA.

XX ABB96876;

XX 12-JUL-2002 (first entry)

XX Omega-conopeptide P6.3 toxin sequence.

KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
KW stroke; cerebrovascular accident; brain trauma; spinal cord trauma;
KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
KW psychosis; anxiety; schizophrenia.

OS Conus purpurascens.

XX WO200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

XX 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
XX Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with
XX voltage gated ion channels e.g. pain, inflammation, neurologic or
XX cardiovascular disorders.

XX Claim 1(a); Page 72; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
XX sequences encoding them, and propeptide sequences. The activity of the
XX peptides of the invention may be described as, analgesic, anticonvulsant,
XX vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
XX antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
XX antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
XX by modulating the activity of voltage gated ion channels. They may be
XX used for treating or preventing disorders associated with voltage gated
XX ion channels such as neurological disorders, e.g. seizure (associated
XX with epilepsy), neurotoxic injury associated with conditions of hypoxia,
XX anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
XX cord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
XX events; pain e.g. migraine; inflammation or cardiovascular disorders.
XX They may also be used for treating psychiatric disorders e.g. psychosis,
XX anxiety or schizophrenia. The analgesic agents of the invention show
XX diminished side effects and toxicity, and are non-addictive. The
XX sequences given in records ABB96807-ABB96905 represent omega-conopeptide
XX toxin sequences

XX Sequence 27 AA;

Query Match 44.1%; Score 71; DB 5; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.64;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CRXNKKCFQHLDDCCSRKC 20
 ID ABB96668 standard; peptide; 72 AA.
 Db 2 CKKTGRKCFPHQKCCGRAC 21

RESULT 76
 ABB96668
 XX AC ABB96668;
 XX DT 12-JUL-2002 (first entry)
 XX DE Omega-conopeptide P6.3 propeptide.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus purpurascens.

PN W0200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

PR 21-JUL-2000; 2000US-0219616P.

PR 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;

DR WPI; 2002-257318/30.

DR N-PSDB; ABL98927.

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.

XX Claim 1(c); Page 56; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96595-ABB96697 represent omega-conopeptide
 CC propeptide sequences

XX Sequence 72 AA;

Query Match 44.1%; Score 71; DB 5; Length 72;
 Best Local Similarity 50.0%; Pred. No. 1.4;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 1 CRXNKKCFQHLDDCCSRKC 20
 Db 47 CKKTGRKCFPHQKCCGRAC 66

RESULT 77

ABB96786

ID ABB96786 standard; peptide; 26 AA.

XX AC ABB96786;

XX 12-JUL-2002 (first entry)

XX Omega-conopeptide S6.2 generic toxin sequence.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus striatus.

XX Key Location/Qualifiers

XX Misc-difference 13

XX /label= OTHER

XX /note= "OTHER is Tyr, 125I-Tyr, mono-iodo-Tyr or di-iodo-Tyr or O-sulpho-Tyr or O-Phospho-Tyr"

XX W0200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US023041.

XX 21-JUL-2000; 2000US-0219616P.

XX 05-FEB-2001; 2001US-0265888P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNETIX INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.

XX Example 2; Page 62; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE;
 DR WPI; 2002-257318/30.
 XX
 PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX
 PS Example 2; Page 56; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, anticonvulsant,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96698-ABB96906 represent omega-conopeptide
 CC generic toxin sequences
 XX
 SQ Sequence 27 AA;
 Query Match 39.8%; Score 64; DB 5; Length 27;
 Best Local Similarity 55.0%; Pred. No. 3.7;
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKC 20
 | : | | | | | | | | | |
 Db 2 CKTXGRKCFXHQKCCGRAC 21
 | : | | | | | | | | | |
 RESULT 80
 ID ABB96874 standard; peptide; 27 AA.
 XX
 AC ABB96874;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide P6.1 toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus purpurascens.
 XX
 PN WO200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US023041.
 XX
 PR 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 PA

PA (COGN-) COGNETIX INC.
 XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 XX Jacobsen R, Jones RM, Cartier GE;
 XX WPI; 2002-257318/30.
 DR
 XX New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurologic or
 PT cardiovascular disorders.
 XX
 PS Claim 1(a); Page 72; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of the
 CC peptides of the invention may be described as, analgesic, anticonvulsant,
 CC vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 CC antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 CC antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 CC by modulating the activity of voltage gated ion channels. They may be
 CC used for treating or preventing disorders associated with voltage gated
 CC ion channels such as neurological disorders, e.g. seizure (associated
 CC with epilepsy), neurotoxic injury associated with conditions of hypoxia,
 CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96807-ABB96905 represent omega-conopeptide
 CC toxin sequences
 XX
 SQ Sequence 27 AA;
 Query Match 39.8%; Score 64; DB 5; Length 27;
 Best Local Similarity 55.0%; Pred. No. 3.7;
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CRXNQKCFQHLDDCCSRKC 20
 | : | | | | | | | | | |
 Db 2 CKTXGRKCFXHQKCCGRAC 21
 | : | | | | | | | | | |
 RESULT 81
 ID ABB96842 standard; peptide; 27 AA.
 XX
 AC ABB96842;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Omega-conopeptide Cr6.3 toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus circumcissus.
 XX
 PN WO200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-US023041.
 XX
 PR 21-JUL-2000; 2000US-0219616P.
 PR 05-FEB-2001; 2001US-0265888P.
 XX
 XX (UTAH) UNIV UTAH RES FOUND.
 PA

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21-JUL-2000; 2000US-0219616P.
05-FEB-2001; 2001US-0265888P.
(UTAH ) UNIV UTAH RES FOUND.
(COGN-) COGNETIX INC.
Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
Jacobsen R, Jones RM, Cartier GE;
WPI; 2002-257318/30.
N-PSDB; ABL9885.
New omega-conopeptides useful for treating disorders associated with
voltage gated ion channels e.g. pain, inflammation, neurologic or
cardiovascular disorders.
Claim 1 (c); Page 36; 195pp; English.
The invention relates to isolated omega-conopeptides, nucleic acid
sequences encoding them, and propeptide sequences. The activity of
peptides of the invention may be described as, analgesic, anticonvulsant,
vasotropic, cardiant, neuroprotective, cerebroprotective, cardiovascular
antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary
antipsychotic, anxiolytic and neuroleptic. Peptides of the invention
used for treating the activity of voltage gated ion channels. They may be
used for treating or preventing disorders associated with voltage gated
ion channels such as neurological disorders, e.g. seizure (associated
with epilepsy), neurotoxic injury associated with conditions of hypox
anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
cord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemia
events; pain e.g. migraine; inflammation or cardiovascular disorders.
They may also be used for treating psychiatric disorders e.g. psychoses
anxiety or schizophrenia. The analgesic agents of the invention show
diminished side effects and toxicity, and are non-addictive. The
sequences given in records AB96595-AB96697 represent omega-conopeptide
propeptide sequences
Sequence 73 AA;
Query Match 39.4%; Score 63.5; DB 5; Length 73;
Best Local Similarity 37.0%; Pred. No. 9.3;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps
QY 1 CRIXNQKCFQHLDDCCSRKCNRFN-KC 26
| : | | : | | | | : | : | : |
db 46 CKSKGAKGSRMLMYDCCSGCSRYSGRC 72
RESULT 83
AAW06589
AAW06589 standard; peptide; 38 AA.
AAW06589;
14-FEB-1997 (first entry)
Tyrosinase inhibitor peptide.
Tyrosinase inhibitor; pupae; house fly; melanin; dermal medicine;
cosmetic; food preservative; insecticide.
Synthetic.
Key Location/Qualifiers
Misc-difference 32
/label= Tyr, OTHER
/note= "OTHER = 3,4-dihydroxyphenylalanine"
JP08231592-A.
10-SEP-1996.
27-FEB-1995; 95JP-00038405.

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(UTAH) UNIV UTAH RES FOUND.
(COGN-) COGNEX INC.

Walker CS, Shetty R, Jiminez EC, McIntosh JM, Olivera BM;
Watkins M, Jones RM, Shen GS;
WPI; 2002-171634/22.

Pure I-conotoxin peptides isolated from venom of cone snails, useful for the regulation of the flow of potassium through potassium channels in the treatment of e.g. multiple sclerosis.

Claim 2; Page 54; 26Opp; English.

The present invention describes substantially pure I-conotoxin peptides of 30 - 50 residues (I). (I) have neuroprotective, antiinflammatory, ophthalmological, antidote, antibacterial, anticonvulsant, muscular, cardiovascular, antiarrhythmic, cardiant, antidiabetic, antiaddictive, immunosuppressive, cytostatic, nootropic, cerebroprotective, relaxant, antiasthmatic, vasotropic, analgesic, antimigraine, antineumatic, antiarthritic, dermatological, tranquiliser and neuroleptic activities. (II) can be used as an H₂Atpase stimulator, potassium agonist and curate antagonist. (I) are useful in the treatment of multiple sclerosis, acute disseminated encephalomyelitis, optic neuromyelitis, progressive acute multifocal leukoencephalopathy, adrenoleukodystrophy, acute transverse myelitis, subacute sclerosing panencephalomyelitis, metachromic leukodystrophy, Pelizaeus-Merzbacher disease, spinal cord injury, botulinum toxin poisoning, Huntington's chorea, compression and entrapment neuropathies, cardiovascular disease, spinal cord injury, hyperglycaemia, immunosuppression, cocaine addiction, reactive gliosis, dysfunction, disorders resulting from the defects of neurotransmitter release and reversal of the actions curate and other neuromuscular blocking drugs. (I) can also be used to treat disorders associated with radical depolarisation of excitable membranes, and disorders associated with voltage gated ion channels, pain and a neuromuscular disorder. (I) are also useful for screening compounds that mimic the activity of an I-conotoxin. They are also useful for the treatment of autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, Alzheimer's, anxiety and schizophrenia. ABL8662 to ABL88778 and ABB88546 to ABB88934 represent sequences used in the exemplification of the present invention

Sequence 73 AA;

Query Match 38.8%; Score 62.5; DB 5; Length 73;
Best Local Similarity 40.7%; Pred. No. 12;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRIXNOKCFOHLDDCSRKCNKRV 27
Db 39 CLSLGORCERH-SDCCGYLCCFYDKCV 64

RESULT 86
ABB96774
ID ABB96774 standard; peptide; 27 AA.
AC ABB96774;
AC ABB96774;
DT 12-JUL-2002 (first entry)
DE Omega-conopeptide P6.3 generic toxin sequence.
XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
KW psychosis; anxiety; schizophrenia.
XX

XX DE Cone snail O-superfamily conotoxin propeptide, Di6.5.
 XX KW Cone snail; O-superfamily conotoxin; sodium channel;
 KW demyelinating disease; multiple sclerosis; Huntington's disease;
 KW neuropathy; carpal tunnel syndrome; cardiovascular disorder;
 KW congestive heart failure; cancer; immunosuppression; epilepsy; asthma;
 KW ischaemia; stroke; pain.
 XX OS Conus distans.
 XX PN WO200149312-A2.
 XX PD 12-JUL-2001.
 XX PF 28-DEC-2000; 2000WO-US035431.
 XX PR 30-DEC-1999; 99US-0173754P.
 XX PR 26-JUN-2000; 2000US-0214263P.
 XX PR 20-JUL-2000; 2000US-0219440P.
 XX PR 27-OCT-2000; 2000US-0243412P.
 XX PA (UTAH) UNIV UTAH RES FOUND.
 XX PA (COGN-) COGNETIX INC.
 XX PI Olivera BM, Cartier GE, Watkins M, Hillyard DR, McIntosh JM;
 PI Layer RT, Jones RM;
 XX DR WPI: 2001-418352/44.
 XX DR N-PSDB; AAS10951.
 XX PT New O-superfamily polypeptides useful for treating voltage gated ion
 PT channel disorders, including demyelinating diseases i.e. multiple
 PT sclerosis.
 XX PS Claim 15; Page 60; 277pp; English.
 XX CC The sequence is a cone snail O-superfamily conotoxin propeptide. The
 CC peptides are useful for regulating the flow of sodium through sodium
 CC channels in an individual and the treatment or prevention of disorders
 CC associated with voltage gated ion channel disorders including
 CC demyelinating diseases i.e. multiple sclerosis, optic neuromyelitis,
 CC disseminated encephalomyelitis, adrenoleukodystrophy, acute transverse
 CC myelitis, progressive multifocal leukoencephalopathy, sub acute
 CC sclerosing panencephalomyelitis (SSPE), metachromatic leukodystrophy,
 CC Pelizaeus-Merzbacher disease, spinal cord injury, botulinum toxin
 CC poisoning, Huntington's, compression, entrapment neuropathies i.e. ulnar
 CC nerve palsy, and carpal tunnel syndrome, cardiovascular disorders, i.e.
 CC cardiac arrhythmias and congestive heart failure, reactive gliosis,
 CC hyperglycaemia, immunosuppression, cocaine addiction, cancer, cognitive
 CC dysfunction, neurotransmitter disorders (i.e. Eaton-Lambert syndrome) and
 CC reversal of curare and other neuromuscular blocking drugs. The
 CC neurological disorder is a seizure, preferably one associated with
 CC epilepsy. The neurological disorder is a neurotoxic injury associated
 CC with hypoxia, anoxia or ischaemia. The neurotoxic injury is associated
 CC with stroke, cerebrovascular accident, brain or spinal cord trauma,
 CC myocardial infarct, physical trauma, drownings, suffocation, perinatal
 CC asphyxia or hypoglycaemic events. The disorder is pain i.e. migraine,
 CC acute pain, persistent pain, neuropathic pain, nociceptive pain. The
 CC disorder is inflammation or a cardiovascular disorder. A conotoxin
 CC peptide is useful to alleviate pain in a mammal in pain or about to be
 CC subjected to a pain causing event, and to treat disorders associated with
 CC radical depolarisation of excitable membranes by activating a KATP
 CC channel, the disorders include cardiac, ocular and cerebral ischaemia and
 CC asthma
 XX SQ Sequence 76 AA;
 Query Match 38.5%; Score 62; DB 4; Length 76;
 Best Local Similarity 39.3%; Pred. No. 14;
 Matches 11; Conservative 6; Mismatches 9; Indels 2; Gaps 2;
 QY 1 CRXNQKQFQHLDDCCSRKNRF-NKCV 27

DB 48 CNEAQEHCTQN-PDCCSECNKRFVGRCL 74

RESULT 88

ABB96741

ID ABB96741 standard; peptide; 27 AA.

XX ABB96741;

AC ABB96741;

XX 12-JUL-2002 (first entry)

XX Omega-conopeptide E6.2 generic toxin sequence.

DE Omega-conopeptide E6.2 generic toxin sequence.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 stroke; cerebrovascular accident; brain trauma; spinal cord trauma;
 drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 psychosis; anxiety; schizophrenia.

XX Conus ermineus.

OS Conus ermineus.

XX Key Location/Qualifiers

XX Misc-difference 1 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 4 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 11 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

FT Misc-difference 27 /label= OTHER

FT /note= "OTHER is Pro or Hydroxy Pro"

WO200207675-A2.

31-JAN-2002.

23-JUL-2001; 2001WO-US023041.

21-JUL-2000; 2000US-0219616P.

05-FEB-2001; 2001US-0265888P.

(UTAH) UNIV UTAH RES FOUND.

(COGN-) COGNETIX INC.

PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX WPI: 2002-257318/30.

XX New omega-conopeptides useful for treating disorders associated with
 voltage gated ion channels e.g. pain, inflammation, neurologic or
 cardiovascular disorders.

XX Example 2; Page 42; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 sequences encoding them, and propeptide sequences. The activity of the
 peptides of the invention may be described as, analgesic, anticonvulsant,
 vasotrophic, cardiant, neuroprotective, cerebroprotective, cardiovascular,
 antiinflammatory, antimigraine, antidiabetic, tranquiliser, vulnerary,
 antipsychotic, anxiolytic and neuroleptic. Peptides of the invention act
 by modulating the activity of voltage gated ion channels. They may be
 used for treating or preventing disorders associated with voltage gated
 ion channels such as neurological disorders, e.g. seizure (associated
 with epilepsy), neurotoxic injury associated with conditions of hypoxia,

CC anoxia, ischaemia, stroke, cerebrovascular accident, brain or spinal
 CC chord trauma, drowning, suffocation, perinatal asphyxia or hypoglycaemic
 CC events; pain e.g. migraine; inflammation or cardiovascular disorders.
 CC They may also be used for treating psychiatric disorders e.g. psychosis,
 CC anxiety or schizophrenia. The analgesic agents of the invention show
 CC diminished side effects and toxicity, and are non-addictive. The
 CC sequences given in records ABB96698-ABB96806 represent omega-conopeptide
 CC generic toxin sequences
 XX Sequence 27 AA;
 SQ

Query Match 38.2%; Score 61.5; DB 5; Length 27;
 Best Local Similarity 47.8%; Pred. No. 6.9;
 Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 XNKCQFQHLDDCCSRKCNFNKC 26
 Db 5 KGRKCFXHQKCCNKTCR-SKC 26

RESULT 89
 AAR39616
 ID AAR39616 standard; peptide; 26 AA.
 XX
 AC AAR39616;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)
 XX
 DE MVIIC/SNX230.
 XX
 KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; WVIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 XX
 PN WO9313128-A1.
 XX
 PD 08-JUL-1993.
 XX
 PF 30-DEC-1992; 92WO-US011349.
 XX
 PR 30-DEC-1991; 91US-00814759.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 XX
 DR WPI; 1993-227270/28.
 XX
 PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.
 XX
 PS Claim 1; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT WVIIA binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct

CC PN field.)
 XX
 SQ Sequence 26 AA;
 Query Match 37.9%; Score 61; DB 2; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
 Db 1 CKKGAPCRKTMWDCCSGCGRRKC 26

RESULT 90
 AAR39617
 ID AAR39617 standard; peptide; 26 AA.
 XX
 AC AAR39617;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-DEC-1993 (first entry)
 XX
 DE SNX231.
 XX
 KW Omega conopeptide; OCT; analgesia; inhibition; voltage-gated;
 KW calcium channel; neurone; contraction; guinea pig; ileum; WVIIA;
 KW binding site; toxin; marine; snail; Conus; opiod; chronic pain;
 KW narcotics.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Modified-site 7 /note= "4Hyp"
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 XX
 PN WO9313128-A1.
 XX
 PD 08-JUL-1993.
 XX
 PF 30-DEC-1992; 92WO-US011349.
 XX
 PR 30-DEC-1991; 91US-00814759.
 XX
 PA (NEUR-) NEUREX CORP.
 XX
 PI Justice A, Singh T, Gohil K, Valentino KL, Miljanich GP;
 XX
 DR WPI; 1993-227270/28.
 XX
 PT Use of omega-cono-peptide(s) which selectively inhibit voltage-gated
 PT calcium channels - to induce analgesia, enhance opiate analgesics, treat
 PT pain etc.
 XX
 PS Claim 1; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR39608-30 are omega conopeptides (OCTs) and
 CC derivatives of these, which may be used to produce analgesia in a mammal.
 CC These OCTs inhibit voltage-gated calcium channels selectively in neuronal
 CC tissue. This is shown by the peptides ability to stimulate contraction in
 CC guinea pig ileum and to bind to OCT WVIIA binding sites present in
 CC neuronal tissue. OCTs are components of peptide toxins derived from
 CC marine snails of the genus Conus, and act as calcium channel blockers.
 CC These OCTs may be used to replace opiods in the treatment of chronic pain
 CC or to reduce the opiod dosage required. This helps to reduce dependence
 CC on and tolerance to opiod narcotics. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 SQ Sequence 26 AA;
 Query Match 37.9%; Score 61; DB 2; Length 26;

Best Local Similarity 38.5%; Pred. No. 7.6; Mismatches 4; Indels 12; Gaps 0;

Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRENKC 26
| : : : : | | | | |
Db 1 CKGKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 91
AAR37762
ID AAR37762 standard; peptide; 26 AA.
XX
AC AAR37762;
XX
DT 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
DE SNX-231.
XX
KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
KW GVIA; GVIIA; RVIA; SVIA; TVIA; SNX-207; stroke; delayed treatment;
KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW N-channel mediated neurotransmitter release.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Disulfide-bond 1. .16
FT Modified-site 7 /note= "hydroxyproline"
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
XX
PN WO9310145-A1.
XX
PD 27-MAY-1993.
XX
PF 12-NOV-1992; 92WO-US009766.
XX
PR 12-NOV-1991; 91US-00789913.
PR 17-JUL-1992; 92US-00916478.
XX
XX (NEUR-) NEUREX CORP.
PA
PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
PI Yamashiro DH;
XX
DR WPI; 1993-182487/22.
XX
PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
PT bind specifically to omega-conotoxin MVIIA binding sites.
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC Ischaemia-related neuronal damage in mammals is reduced by admin.; 4-24
CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
CC damage caused by stroke. By delaying admin. for some time (compare
CC US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a
CC greater redn. in neuronal damage is achieved. (I) is admin. e.g. by
CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
CC in blood pressure caused by (I)). (I) is also at least as effective as
CC the specified conotoxins for (1) selective inhibition of N-type voltage-
CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
CC channel mediated neurotransmitter release in neuronal tissue. Primary
CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

SQ Sequence 26 AA;
Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 7.6;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRENKC 26
| : : : : | | | | |
Db 1 CKGKGAPCRKTMWDCCSGCGRRGKC 26

RESULT 92
AAR37761
ID AAR37761 standard; peptide; 26 AA.
XX
AC AAR37761;
XX
DT 25-MAR-2003 (revised)
DT 08-SEP-1993 (first entry)
XX
DE MVIIC/SNX-230.
XX
KW Ischaemia; neuronal; omega-conotoxin; OCT; MVIIA; MVIIC; MVIID; MVIIB;
KW GVIA; GVIIA; RVIA; SVIA; TVIA; SNX-207; stroke; delayed treatment;
KW antihistamine; blood pressure; N-type voltage-gated Ca currents;
KW N-channel mediated neurotransmitter release.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Disulfide-bond 1. .16
FT Disulfide-bond 8. .20
FT Disulfide-bond 15. .26
XX
PN WO9310145-A1.
XX
PD 27-MAY-1993.
XX
PF 12-NOV-1992; 92WO-US009766.
XX
PR 12-NOV-1991; 91US-00789913.
PR 17-JUL-1992; 92US-00916478.
XX
XX (NEUR-) NEUREX CORP.
PA
PI Miljanich GP, Bowersox SS, Fox JA, Valentino KL, Bitner RS;
PI Yamashiro DH;
XX
DR WPI; 1993-182487/22.
XX
PT Redn. of neuronal damage caused by ischaemia - by admin. of cpds. that
PT bind specifically to omega-conotoxin MVIIA binding sites.
XX
PS Disclosure; Fig 1; 103pp; English.
XX
CC Ischaemia-related neuronal damage in mammals is reduced by admin.; 4-24
CC hr after onset of ischaemia, of a cpd. (I) which binds selectively to an
CC omega-conotoxin (OCT) MVIIA site in neuronal tissue. (I) has selectivity
CC at least 100 expressed as ratio of binding affinity for the MVIIA site to
CC that for the MVIIC site. (I) is one of the OCTs MVIIA, MVIIB, GVIA, GVIIA
CC or RVIA or it is the cpd. SNX-207. (I) is esp. used to reduce neuronal
CC damage caused by stroke. By delaying admin. for some time (compare
CC US5051403 where cpds. are given within 1 hr of the onset of ischaemia) a
CC greater redn. in neuronal damage is achieved. (I) is admin. e.g. by
CC intracerebroventricular (ICV) injection at 0.1-20 microg/kg, but can also
CC be given i.v. (opt. after treatment with antihistamines to minimise redn.
CC in blood pressure caused by (I)). (I) is also at least as effective as
CC the specified conotoxins for (1) selective inhibition of N-type voltage-
CC gated Ca currents in neuronal tissue and (2) selective inhibition of N-
CC channel mediated neurotransmitter release in neuronal tissue. Primary
CC sequences of omega-conopeptides are given in AAR37752-62. Several analog
CC omega-conopeptides are given in AAR37763-76. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX

XX SQ Sequence 26 AA;

Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. NO. 7.6;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
| : | : | : | : ||
DB 1 CKGGAPCRKTMVDCCSGCGRGKC 26

RESULT 93
AAW19552
ID AAW19552 standard; peptide; 26 AA.
XX AC
XX AAW19552;
DT 27-AUG-2003 (revised)
DT 13-OCT-1997 (first entry)
DE Natural omega-conopeptide MWIIC/SNX-230 used for pain relief.
XX Conopeptide; cone snail; pain; analgesic; neuropathy; epidural;
KW N-type voltage-sensitive calcium channel; block; Conus.
OS Conus.
XX WO9701351-Al.
XX PD 16-JAN-1997.
XX PF 26-JUN-1996; 96WO-US011041.
XX PR 27-JUN-1995; 95US-00496847.
PR 08-MAR-1996; 95US-00613400.
PA (NEUR-) NEUREX CORP.
XX AMstutz GA, Bowersox SS, Gohil K, Adriaenssens PI, Kristipati R;
PI Gadbois T, Pettus MR, Luther RR;
XX WPI; 1997-100012/09.

Stable omega conopeptide compositions - for producing analgesia and for inhibiting progression of neuropathic pain disorders.

Disclosure; Fig 2; 47pp; English.

AAW19544-W19553 are naturally occurring omega conopeptides (OCs) isolated from Conus sp. (cone snails). The peptides and their analogues are used as analgesics acting by blocking N-type voltage-sensitive calcium channels. The OCs can be used to treat neuropathic pain as a result of e.g. insult to the spinal cord or peripheral nerves, cancer, bone degenerative diseases, AIDS, reflex sympathetic dystrophy, herpes zoster neuropathy, diabetic neuropathy, hyperesthesia, allodynia or hyperalgesia. The OCs are preferably administered in a medicament via an epidural route in a continuous infusion or sustained release formulation. The OCs can provide pain relief when administered epidurally in the absence of a permeation enhancer, at doses that are comparable to effective analgesic doses using intrathecal administration. OC formulations comprising an OC and a carboxylic acid buffer anti-oxidant. They also confer stability to solutions containing them for prolonged treatment methods and long-term storage. (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 26 AA;

Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. NO. 7.6;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

OY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26


```

PR 15-APR-1993; 93US-00049794.
PR 03-JUL-1996; 96US-00675354.
PR 01-NOV-1996; 96US-00742774.
XX
PA (ELAN-) ELAN PHARM INC.
XX
PI Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
XX WPI; 2000-038270/03.
XX
XX Measuring the activity of test compounds in blocking voltage-gated
XX calcium channels, binding to the omega conopeptide binding site and
XX inhibiting norepinephrine (noradrenaline) release for treating
XX inflammation.
XX
XX Disclosure; Fig 1; 47pp; English.
XX
XX A method has been developed of selecting a test compound for treating
XX inflammation. The method comprises measuring the activity of the test
XX compound in blocking voltage-gated calcium channels, binding to the omega
XX conopeptide binding site and inhibiting norepinephrine (noradrenaline)
XX release from nervous tissue. The method is useful for selecting compounds
XX for treating inflammation. The selected compounds are capable of
XX producing analgesia in a mammalian subject with chronic or intractable
XX pain. Analgesia caused by selected compounds may reduce the reliance on
XX opioid analgesic agents of the prior art which cause dependency and
XX tolerance, requiring potentially dangerous increases in opioid doses to
XX achieve the analgesic effect. The present sequence represents an omega
XX conopeptide given in the present invention
XX
XX Sequence 26 AA;
XX
XX Query Match 37.9%; Score 61; DB 3; Length 26;
XX Best Local Similarity 38.5%; Pred. No. 7.6;
XX Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0
QY 1 CRXNQCFQHLDDCCSRKGNRFNKC 26
Db |: : : : : : : : : :
1 CKGKGAPCRKTWYDCSGSGCRGKC 26
RESULT 99
AAAY43715
ID AAY43715 standard; peptide; 26 AA.
XX
XX AAY43715;
XX
XX 11-FEB-2000 (first entry)
XX
XX Amino acid sequence of an omega-conotoxin MWIIC.
XX
XX Omega-conotoxin; venom; predatory marine snail; N-type calcium channel;
XX neuronal damage reduction; ischemia; analgesia; opiate analgesia;
XX schizophrenia; stimulant induced psychosis; hypertension; inflammation;
XX bronchoconstriction; neuropathic pain; voltage sensitive calcium channel.
XX
XX Conus magus.
XX
XX OS
XX
XX WO9954350-A1.
XX
XX 28-OCT-1999.
XX
XX
XX 16-APR-1999; 99WO-AU000288.
XX
XX 16-APR-1998; 98AU-00002989.
XX
XX 01-FEB-1999; 99AU-00008419.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Drinkwater RD, Lewis RJ, Alewood PF, Nielsen KJ;
XX WPI; 2000-013226/01.
XX
XX

```

PT Novel peptides used for the treatment of disorders and diseases where
 XX blockage of the N-type calcium channels is required.
 PS Disclosure; Page 12; 81pp; English.
 CC The present sequence represents an omega-conotoxin. Omega-conotoxins are
 CC isolated from venoms of predatory marine snails, and have a selectivity
 CC for N-type calcium channels over P/Q type channels, and so block N-type
 CC calcium channels. The omega-conotoxins of the invention can be used in
 CC any disease or disorder where blockage of N-type calcium channels is
 CC required, e.g. in the reduction of neuronal damage following ischemia,
 CC production of analgesia, or enhancement of opiate analgesia, in the
 CC treatment of schizophrenia, stimulant induced psychoses, hypertension,
 CC inflammation, and diseases which cause bronchotension, and also in the
 CC inhibition of progression of neuropathic pain. They can also be used in a
 CC screen to identify compounds with activity at N-type voltage sensitive
 CC calcium channels
 XX Sequence 26 AA;
 SQ Query Match 37.9%; Score 61; DB 3; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 : : : : :
 Db 1 CKGKGAPCRKTMVDCSGSGRRGKC 26
 : : : : :
 RESULT 100
 AAB14377
 ID AAB14377 standard; peptide; 26 AA.
 XX
 AC AAB14377;
 XX
 DT 06-DEC-2000 (first entry)
 XX
 DE Omega-conopeptide MVIIC/SNX-230.
 XX
 KW Marine snail; omega-conopeptide; calcium channel blocker; MVIIC; SNX-230;
 KW toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic;
 KW norepinephrine release inhibitor; schizophrenia; tardive dyskinesia;
 KW acute dystonic reaction; inflammation; epilepsy.
 XX
 OS Conus sp.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..16
 FT Disulfide-bond 8..20
 FT Disulfide-bond 15..26
 FT Modified-site 26
 FT /note= "C-terminal amide"
 XX
 PN US6087091-A.
 XX
 PD 11-JUL-2000.
 XX
 XX 23-APR-1999; 99US-00298017.
 PF
 XX 30-DEC-1991; 91US-00814759.
 PR 15-APR-1993; 93US-00049794.
 PR 03-JUL-1996; 96US-00675354.
 PR 01-NOV-1996; 96US-00742774.
 PR 21-AUG-1998; 98US-00138439.
 XX
 PA (ELAN-) ELAN PHARM INC.
 XX
 PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX
 DR WPI; 2000-490177/43.
 XX
 XX Selecting a compound for producing analgesia involves measuring activity
 PT of test compound in blocking voltage-gated calcium channels, binding to

PT omega conopeptide binding site and inhibiting norepinephrine release.
 XX Disclosure; Fig 1; 58pp; English.
 CC The present sequence is an omega-conopeptide from marine snails of the
 CC genus Conus. Omega-conopeptides are components of peptide toxins produced
 CC by the cone snails, and which act as calcium channel blockers. Natural
 CC omega-conopeptides and their derivatives may be useful for producing
 CC analgesia in nociceptive and neuropathic pain. The peptides bind to omega
 CC -conopeptide binding sites, which are present mainly in neuronal tissue,
 CC and inhibit norepinephrine release from nervous tissue. Conopeptides such
 CC as MVIIC and TVIIC are effective as therapeutic agents for treating
 CC neurogenic conditions such as schizophrenia, tardive dyskinesia and acute
 CC dystonic reactions, inflammation and epilepsy
 XX Sequence 26 AA;
 SQ Query Match 37.9%; Score 61; DB 3; Length 26;
 Best Local Similarity 38.5%; Pred. No. 7.6;
 Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;
 OY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
 : : : : :
 Db 1 CKGKGAPCRKTMVDCSGSGRRGKC 26
 : : : : :
 Search completed: April 18, 2005, 20:33:44
 Job time : 126.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:24:17 ; Search time 30.5 Seconds
(without alignments)
66.083 Million cell updates

Title: US-10-627-685A-26
Perfect score: 161
Sequence: 1 CRXNOKCFQHLDDCCSRKCNRFNKCVC 27

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length:

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Maximum DB seq length: 9
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100

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Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
6: /cgn2_6/ptodata/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	SUMMARIES	
						Description	
1	161	100.0	27	1	US-08-619-936-1	Sequence 1, Appli	
2	75	46.6	26	1	US-07-789-913-19	Sequence 19, Appl	
3	75	46.6	26	1	US-08-049-794-19	Sequence 19, Appl	
4	75	46.6	26	1	US-08-496-847-19	Sequence 19, Appl	
5	75	46.6	26	2	US-08-742-774-19	Sequence 19, Appl	
6	75	46.6	26	2	US-08-675-354-19	Sequence 19, Appl	
7	75	46.6	26	2	US-08-965-918-19	Sequence 19, Appl	
8	75	46.6	26	2	US-09-138-439-19	Sequence 19, Appl	
9	75	46.6	26	3	US-08-613-400A-19	Sequence 19, Appl	
10	75	46.6	26	3	US-09-298-017-19	Sequence 19, Appl	
11	75	46.6	26	3	US-09-392-979A-19	Sequence 19, Appl	
12	71	44.1	26	1	US-07-789-913-8	Sequence 8, Appli	
13	71	44.1	26	1	US-08-049-794-8	Sequence 8, Appli	
14	71	44.1	26	1	US-08-496-847-8	Sequence 8, Appli	
15	71	44.1	26	2	US-08-742-774-8	Sequence 8, Appli	
16	71	44.1	26	2	US-08-675-354-8	Sequence 8, Appli	
17	71	44.1	26	2	US-08-965-918-8	Sequence 8, Appli	
18	71	44.1	26	2	US-09-138-439-8	Sequence 8, Appli	
19	71	44.1	26	3	US-08-613-400A-8	Sequence 8, Appli	
20	71	44.1	26	3	US-09-298-017-8	Sequence 8, Appli	
21	71	44.1	26	3	US-09-392-979A-8	Sequence 8, Appli	
22	62.5	38.8	36	4	US-09-894-882-369	Sequence 369, App	
23	62.5	38.8	36	4	US-09-894-882-167	Sequence 167, App	
24	62	38.5	76	4	US-09-749-637A-207	Sequence 207, App	
25	61	37.9	26	1	US-08-049-794-29	Sequence 29, Appl	
26	61	37.9	26	1	US-08-496-847-29	Sequence 29, Appl	
27	61	37.9	26	2	US-08-742-774-29	Sequence 29, Appl	

ALIGNMENTS

RESULT 1

US-08-619-936-1
; Sequence 1, Application US/08619936
; Patent No. 5672682
; GENERAL INFORMATION:
; APPLICANT: Terlau, Heinrich
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Grille, Michelle
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Conotoxin Peptide PVIIA
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/619,936
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 24260-107574-04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "4Hyp"
; OTHER INFORMATION: /note= "Amino acid 4 may be 4-trans-hydroxyproline."
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 1..16
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 8..20
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: 15..26
US-08-619-936-1

Query Match 100.0%; Score 161; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27

RESULT 2

US-07-789-913-19
; Sequence 19, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-202
US-07-789-913-19

Query Match 46.6%; Score 75; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.023;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
DB 1 CKLKGQCSRLMYDCCSGCGSGKC 26

RESULT 3

US-08-049-794-19
; Sequence 19, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C

Query Match 44.1%; Score 71; DB 1; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-742-774-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
|:::|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCRKTSYDCSCGSGRSKC 26

RESULT 16
US-08-675-354-8
; Sequence 8, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Deklinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-742-774-8
```

```
;
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-675-354-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
|:::|:::|:::|:::|:::|:::|:::|
Db 1 CKLKGQSCRKTSYDCSCGSGRSKC 26

RESULT 17
US-08-965-918-8
; Sequence 8, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
; US-08-965-918-8
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Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 18

US-09-138-439-8

; Sequence 8, Application US/09138439

; Patent No. 5994305

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/138,439

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/049,794

; FILING DATE: 1993-04-15

; APPLICATION NUMBER: US 07/814,759

; FILING DATE: 30-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0009.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0960

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1

US-09-138-439-8

Query Match 44.1%; Score 71; DB 2; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 19

US-08-613-400A-8

; Sequence 8, Application US/08613400A

; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-08-613-400A-8

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CRXNKCFOHLDCCSRKCNFNKC 26
Db 1 CKLGQSCRKTSYDCCSGSGRSKC 26

RESULT 20

US-09-298-017-8

; Sequence 8, Application US/09298017

; Patent No. 6087091

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

```

; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-298-017-8

```

```

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

```

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
DB 1 CLKGQSCRKTSYDCSCGSGRSGKC 26

```

```

RESULT 21
US-09-392-979A-8
; Sequence 8, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Deklinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15

```

```

; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SVIB/SNX-183, FIGURE 1
US-09-392-979A-8

```

```

Query Match 44.1%; Score 71; DB 3; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.065;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

```

```

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 26
DB 1 CLKGQSCRKTSYDCSCGSGRSGKC 26

```

```

RESULT 22
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Oliveira, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

```

```

Query Match 38.8%; Score 62.5; DB 4; Length 36;
Best Local Similarity 40.7%; Pred. No. 0.8;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

```

```

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKC 27
DB 2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27

```



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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/675,354
/ FILING DATE: 03-JUL-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/049,794
/ FILING DATE: 1993-APR-15
/ APPLICATION NUMBER: US 07/814,759
/ FILING DATE: 30-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stratford, Carol A.
/ REGISTRATION NUMBER: 34,444
/ REFERENCE/DOCKET NUMBER: 5865-0009.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
/ US-08-675-354-29

Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
   | : | : | : | : | : | : | :
Db 1 CKKGAPCRKTYDCCSGCGRRGKC 26

RESULT 29
US-08-965-918-29
/ Sequence 29, Application US/08965918
/ Patent No. 5891849
/ GENERAL INFORMATION:
/ APPLICANT: Ametutz, Gary A.
/ APPLICANT: Bowersox, Stephen S.
/ APPLICANT: Gohil, Kishorchandra
/ APPLICANT: Adriaenssens, Peter I.
/ APPLICANT: Kristipati, Ramasharma
/ TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
/ PROGRESSION OF NEUROPATHIC PAIN
/ NUMBER OF SEQUENCES: 36
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dehlinger & Associates
/ STREET: 350 Cambridge Avenue, Suite 250
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94306-1546
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/965,918
/ FILING DATE: 07-NOV-1997
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mohr, Judy M.
/ REGISTRATION NUMBER: 38,563
/ REFERENCE/DOCKET NUMBER: 5865-0009.34
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-324-0880
```

```
/ TELEFAX: 650-324-0960
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
/ US-08-965-918-29

Query Match 37.9%; Score 61; DB 2; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
   | : | : | : | : | : | : | :
Db 1 CKKGAPCRKTYDCCSGCGRRGKC 26

RESULT 30
US-09-138-439-29
/ Sequence 29, Application US/09138439
/ Patent No. 5994305
/ GENERAL INFORMATION:
/ APPLICANT: JUSTICE, ALAN
/ APPLICANT: SINGH, TEJINDER
/ APPLICANT: GOHIL, KISHOR C
/ APPLICANT: VALENTINO, KAREN L
/ APPLICANT: MILJANICH, GEORGE P
/ TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
/ ENHANCING OPIATE ANALGESIA
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Law Offices of Peter Dehlinger
/ STREET: 350 Cambridge Avenue, Suite 300
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/138,439
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/049,794
/ FILING DATE: 1993-04-15
/ APPLICATION NUMBER: US 07/814,759
/ FILING DATE: 30-DEC-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stratford, Carol A.
/ REGISTRATION NUMBER: 34,444
/ REFERENCE/DOCKET NUMBER: 5865-0009.30
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 26 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
/ US-09-138-439-29
```

100

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-230, FIGURE 1
; US-09-392-979A-29

Query Match 37.9%; Score 61; DB 3; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.89;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : | : | : | : | : | : | : |
Db 1 CKGGAPCRKTMVDCSCGCGRRGKC 26

RESULT 34
US-09-092-215-9
; Sequence 9, Application US/08092215
; Patent No. 5591821
; GENERAL INFORMATION:
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Julia S.
; APPLICANT: Monje, Virginia D.
; TITLE OF INVENTION: w-Conotoxin Peptides
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092,215
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ihnen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24260-107674
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
```

```
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-092-215-9

Query Match 37.9%; Score 61; DB 1; Length 29;
Best Local Similarity 38.5%; Pred. No. 0.97;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
   | : | : | : | : | : | : | : |
Db 3 CKGGAPCRKTMVDCSCGCGRRGKC 28

RESULT 35
US-09-191-647-9
; Sequence 9, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brosse, Katja
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; CURRENT FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; EARLIER FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; US-09-191-647-9

Query Match 36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 27
   | : | : | : | : | : | : | : |
Db 254 CEKNIDDCVNSKCGGKCV 273

RESULT 36
US-09-540-245A-9
; Sequence 9, Application US/09540245A
; Patent No. 6270984
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brosse, Katja
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,245A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
```

```
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-245A-9

Query Match      36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKCVCV 27
DB 254 CEKNIDCVNSKENGKVCV 273

RESULT 37
US-09-540-153-9
; Sequence 9, Application US/09540153
; Patent No. 6270995
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/540,153
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/191,647
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-153-9

Query Match      36.6%; Score 59; DB 3; Length 735;
Best Local Similarity 45.0%; Pred. No. 28;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKCVCV 27
DB 254 CEKNIDCVNSKENGKVCV 273

RESULT 38
US-09-894-882-365
; Sequence 365, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 365
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-365

Query Match      35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 2 CLSLGQRCGRH-SNCCGYLCCFYDKVCV 27

RESULT 40
US-09-894-882-371
; Sequence 371, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
```

```
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 371
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-371

Query Match          35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFKCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27

RESULT 41
US-09-894-882-372
; Sequence 372, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 372
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-372

Query Match          35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFKCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27

RESULT 41
US-09-894-882-372
; Sequence 372, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 372
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-372
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; ORGANISM: Conus betulinus
US-09-894-882-372

Query Match          35.7%; Score 57.5; DB 4; Length 36;
Best Local Similarity 37.0%; Pred. No. 2.9;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFKCV 27
Db 2 CLSLGQRCERH-SNCCGYLCCFYDKCV 27

RESULT 42
US-09-894-882-155
; Sequence 155, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 155
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-155

Query Match          35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNOKCFQHLDDCCSRKCNRFKCV 27
Db 39 CLSLGQRCERH-SNCCGYLCCFYDKCV 64

RESULT 43
US-09-894-882-164
; Sequence 164, Application US/09894882
; Patent No. 6767895
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
```

;/ TITLE OF INVENTION: I-Superfamily Conotoxins
;/ FILE REFERENCE: 2314-238
;/ CURRENT APPLICATION NUMBER: US/09/894,882
;/ CURRENT FILING DATE: 2001-06-29
;/ PRIOR APPLICATION NUMBER: US 60/
;/ PRIOR FILING DATE: 2000-06-30
;/ PRIOR APPLICATION NUMBER: US 60/243,410
;/ PRIOR FILING DATE: 2000-10-27
;/ PRIOR APPLICATION NUMBER: US 60/246,581
;/ PRIOR FILING DATE: 2000-11-08
;/ PRIOR APPLICATION NUMBER: US 60/247,714
;/ PRIOR FILING DATE: 2000-11-14
;/ PRIOR APPLICATION NUMBER: US 60/264,256
;/ PRIOR FILING DATE: 2001-01-29
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 164
;/ LENGTH: 73
;/ TYPE: PRT
;/ ORGANISM: Conus betulinus
US-09-894-882-164

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 44
US-09-894-882-173
;/ Sequence 173, Application US/09894882
;/ Patent No. 6767895
;/ GENERAL INFORMATION:
;/ APPLICANT: University of Utah Research Foundation
;/ APPLICANT: Cognetix, Inc.
;/ APPLICANT: Walker, Craig S.
;/ APPLICANT: Shetty, Reshma
;/ APPLICANT: Jimenez, Elsie C.
;/ APPLICANT: McIntosh, J. Michael
;/ APPLICANT: Olivera, Baldomero M.
;/ APPLICANT: Watkins, Maren
;/ APPLICANT: Jones, Robert M.
;/ APPLICANT: Shen, Greg S.
;/ TITLE OF INVENTION: I-Superfamily Conotoxins
;/ FILE REFERENCE: 2314-238
;/ CURRENT APPLICATION NUMBER: US/09/894,882
;/ CURRENT FILING DATE: 2001-06-29
;/ PRIOR APPLICATION NUMBER: US 60/
;/ PRIOR FILING DATE: 2000-06-30
;/ PRIOR APPLICATION NUMBER: US 60/243,410
;/ PRIOR FILING DATE: 2000-10-27
;/ PRIOR APPLICATION NUMBER: US 60/246,581
;/ PRIOR FILING DATE: 2000-11-08
;/ PRIOR APPLICATION NUMBER: US 60/247,714
;/ PRIOR FILING DATE: 2000-11-14
;/ PRIOR APPLICATION NUMBER: US 60/264,256
;/ PRIOR FILING DATE: 2001-01-29
;/ NUMBER OF SEQ ID NOS: 506
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 173
;/ LENGTH: 73
;/ TYPE: PRT
;/ ORGANISM: Conus betulinus
US-09-894-882-173

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

Db 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 45
US-09-894-882-176
;/ Sequence 176, Application US/09894882
;/ Patent No. 6767895
;/ GENERAL INFORMATION:
;/ APPLICANT: University of Utah Research Foundation
;/ APPLICANT: Cognetix, Inc.
;/ APPLICANT: Walker, Craig S.
;/ APPLICANT: Shetty, Reshma
;/ APPLICANT: Jimenez, Elsie C.
;/ APPLICANT: McIntosh, J. Michael
;/ APPLICANT: Olivera, Baldomero M.
;/ APPLICANT: Watkins, Maren
;/ APPLICANT: Jones, Robert M.
;/ APPLICANT: Shen, Greg S.
;/ TITLE OF INVENTION: I-Superfamily Conotoxins
;/ FILE REFERENCE: 2314-238
;/ CURRENT APPLICATION NUMBER: US/09/894,882
;/ CURRENT FILING DATE: 2001-06-29
;/ PRIOR APPLICATION NUMBER: US 60/
;/ PRIOR FILING DATE: 2000-06-30
;/ PRIOR APPLICATION NUMBER: US 60/243,410
;/ PRIOR FILING DATE: 2000-10-27
;/ PRIOR APPLICATION NUMBER: US 60/246,581
;/ PRIOR FILING DATE: 2000-11-08
;/ PRIOR APPLICATION NUMBER: US 60/247,714
;/ PRIOR FILING DATE: 2000-11-14
;/ PRIOR APPLICATION NUMBER: US 60/264,256
;/ PRIOR FILING DATE: 2001-01-29
;/ NUMBER OF SEQ ID NOS: 506
;/ SOFTWARE: PatentIn version 3.0
;/ SEQ ID NO 176
;/ LENGTH: 73
;/ TYPE: PRT
;/ ORGANISM: Conus betulinus
US-09-894-882-176

Query Match 35.7%; Score 57.5; DB 4; Length 73;
Best Local Similarity 37.0%; Pred. No. 5.5;
Matches 10; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 39 CLSLGQRCGRH-SNCCGYLCCFYDKCV 64

RESULT 46
US-08-185-432-18
;/ Sequence 18, Application US/08185432
;/ Patent No. 5750652
;/ GENERAL INFORMATION:
;/ APPLICANT: Artavanis-Tsakonas, Spyridon
;/ APPLICANT: Buseau, Isabelle
;/ APPLICANT: Diederich, Robert J.
;/ APPLICANT: Xu, Tian
;/ APPLICANT: Matsuno, Kenji
;/ TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
;/ TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
;/ NUMBER OF SEQUENCES: 23
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: PENNIE & EDMONDS
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible


```

US-09-121-457-3
; Sequence 3, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: QI, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899
; EARLIER FILING DATE: 1997-07-23

```

Qy 1 CRYNQKCFQHLDDCCSRK--CNFEN-KCV 27
| :: : ||| ||| ||| ||| |||
Db 703 CSMGTDNIITYHDDCNRSKSOGNENGKCV 732

```
RESULT 50
US-08-569-214-5
; Sequence 5, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-569-214-5
; Query Match 35.1%; Score 56.5; DB 3; Length 1292;
; Best Local Similarity 43.3%; Pred. No. 88;
; Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNIITYHDDCNRSKQCGNFNGKCV 747

RESULT 51
US-08-569-214-6
; Sequence 6, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,214
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06890
; FILING DATE: 17-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 9148-0006.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-214-5
; Query Match 35.1%; Score 56.5; DB 3; Length 1292;
; Best Local Similarity 43.3%; Pred. No. 88;
; Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNIITYHDDCNRSKQCGNFNGKCV 747

RESULT 52
US-08-937-236-5
; Sequence 5, Application US/08937236
; Patent No. 6187310
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; APPLICANT: DODSON, JAMES M.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MULTIGENE FAMILY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,236
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,214
; FILING DATE: 16 SEPTEMBER 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 291482000622
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1292 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-236-5

Query Match 35.1%; Score 56.5; DB 3; Length 1292;
Best Local Similarity 43.3%; Pred. No. 88;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDNIIYHDDCNSRKSCQGNFGKCV 747

RESULT 53
US-09-641-612-5
; Sequence 5, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.498
; CURRENT APPLICATION NUMBER: US/09/641.612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 585
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(585)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-641-612-5

Query Match 34.8%; Score 56; DB 4; Length 585;
Best Local Similarity 37.9%; Pred. No. 50;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

QY 1 CR--IXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 377 CRAGFAGPRCEHLDLDDCGRACANAGTCV 405

RESULT 54
US-08-185-432-19
; Sequence 19, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Buseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Mateuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-3090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2703 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-19

Query Match 34.8%; Score 56; DB 1; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 822 TGQKCTNIDDCVTNFCNGGTCTI 845

RESULT 55
US-08-899-232-4
; Sequence 4, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2703
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-08-899-232-4

Query Match 34.8%; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 822 TGQKCTNIDDCVTNFCNGGTCTI 845

RESULT 56
US-09-121-457-4
; Sequence 4, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
```

EARLIER FILING DATE: 1997-07-23
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 2703
TYPE: PRT
ORGANISM: Drosophila sp.
US-09-121-457-4

Query Match 34.8%; Score 56; DB 4; Length 2703;
Best Local Similarity 33.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 4 XNOKCFHLDCCSRKCNRFKNCV 27
Db 822 TQCKETNIDCVTPCGNGGTCTI 845

RESULT 57
US-07-689-693B-2
Sequence 2, Application US/07689693B
Patent No. 5231011
GENERAL INFORMATION:

APPLICANT: David Hillyard
APPLICANT: Balomero M. Olivera
TITLE OF INVENTION: Segregated Folding Determinants
TITLE OF INVENTION: for Small Disulfide-Rich Peptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thorpe, No. 5231011th & Western
STREET: 9035 South 700 East, Suite 200
CITY: Sandy
STATE: Utah
COUNTRY: USA
ZIP: 84070

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
COMPUTER: Compaq LTE/286
OPERATING SYSTEM: DOS 4.01
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/689,693B
FILING DATE: 19910418
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
FILING DATE: na

ATTORNEY/AGENT INFORMATION:
NAME: Western, M. Wayne
REGISTRATION NUMBER: 22,788
REFERENCE/DOCKET NUMBER: 9925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 566-8633
TELEFAX: (801) 566-0750

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACIDS

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: MVIIB Omega conotoxin.

IDENTIFICATION METHOD: Direct peptide

IDENTIFICATION METHOD: sequencing of purified Conus magus venom

Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNOKCFHLDCCSRKCNRFKNC 26
Db 1 CKGKGASCHRTSYDCTGSCNR-GKC 25

RESULT 58

US-07-789-913-2
Sequence 2, Application US/07789913
Patent No. 5559095
GENERAL INFORMATION:

APPLICANT: Miljanich, George P.
APPLICANT: Bowersox, Stephen S.
APPLICANT: Fox, James A.
APPLICANT: Valentino, Karen L.
APPLICANT: Bitner, Robert S.
APPLICANT: Yamashiro, Donald H.

TITLE OF INVENTION: Delayed Treatment Method of Reducing
TITLE OF INVENTION: Ischemia-Related Neuronal Damage
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Peter Dehlinger

STREET: 350 Cambridge Avenue, Suite 300

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94306

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/789,913

FILING DATE: 19911112

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/561,766

FILING DATE: 02-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/440,094

FILING DATE: 22-NOV-1989

ATTORNEY/AGENT INFORMATION:

NAME: Stratford, Carol A.

REGISTRATION NUMBER: 34,444

REFERENCE/DOCKET NUMBER: 5865-0005.30

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: AMINO ACID

TOPOLOGY: both

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

INDIVIDUAL ISOLATE: SNX-159

US-07-789-913-2

Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNOKCFHLDCCSRKCNRFKNC 26
Db 1 CKGKGASCHRTSYDCTGSCNR-GKC 25

RESULT 59

US-08-049-794-2
Sequence 2, Application US/08049794
Patent No. 5587454
GENERAL INFORMATION:

APPLICANT: JUSTICE, ALAN

APPLICANT: SINGH, TEJINDER

```

RESULT 60
US-08-496-847-2
; Sequence 2, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATION FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVLIB/SNX-159, FIGURE 1
; US-08-496-847-2

Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels

QY i CRIXNQKCFOHLDDCCSRKNRPNKC 26
   | : | : | : | : | : | : | : |
Db 1 CKGKGASCHRTSYDCCTGSCNR-GKC 25

RESULT 61
US-08-742-774-2
; Sequence 2, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.

```

```

; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MWIIB/SNX-159, FIGURE 1
; US-08-675-354-2

Query Match      34.5%; Score 55.5; DB 2; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels

QY      1 CRIXNQKCFQHLDDCCSRKKNRNFKC 26
      | : | : | : | : | : | : | : |
Db      1 CKKGASCHRTSYDCTGSCNR-GKC 25

RESULT 63
US-08-965-918-2
; Sequence 2, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009,34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MWIIB/SNX-159, FIGURE 1
; US-08-965-918-2

Query Match      34.5%; Score 55.5; DB 2; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1

QY      1 CRIXNQKCFQHLDDCCSRKKNRNFKC 26
      | : | : | : | : | : | : | : |
Db      1 CKKGASCHRTSYDCTGSCNR-GKC 25

RESULT 64
US-09-039-168-2
; Sequence 2, Application US/09039168
; Patent No. 5965534

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Query Match 34.5%; Score 55.5; DB 3; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;


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; FILING DATE: 22-NOV-1989
;SEQ ID NO:2:
; LENGTH: 25
5424218-2

Query Match          34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
       |:| :| :| | :||| || 
Db      1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 72
5189020-1
; Patent No. 5189020
; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox, Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald H.; Tsukokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/561,766
;   FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 440,094
;   FILING DATE: 22-NOV-1989
; SEQ ID NO:1:
; LENGTH: 25
5189020-1

Query Match          34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
       |:| :| :| | :||| || 
Db      1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 70
5189020-2
; Patent No. 5189020
; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox, Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald H.; Tsukokawa, Makoto
; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING OMEGA CONOTOXIN PEPTIDES
; NUMBER OF SEQUENCES: 29
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/561,766
;   FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 440,094
;   FILING DATE: 22-NOV-1989
; SEQ ID NO:2:
; LENGTH: 25
5189020-2

Query Match          34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
       |:| :| :| | :||| || 
Db      1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 71
5424218-2
; Patent No. 5424218
; APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX, STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/147,714
;   FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 855,269
;   FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
;   FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094
```

```
; FILING DATE: 22-NOV-1989
;SEQ ID NO:2:
; LENGTH: 25
5424218-2

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY    1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
     |: | :| ||||| 
Db    1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 72
5189020-1
;Patent No. 5189020
;APPLICANT: Miljanich, George P.;Bitner, Robert S.;Bowersox, Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald H.;Tsubokawa, Makoto
;TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING OMEGA CONOTOXIN PEPTIDES
;NUMBER OF SEQUENCES: 29
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/561,766
;FILING DATE: 02-AUG-1990
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 440,094
;FILING DATE: 22-NOV-1989
;SEQ ID NO:1:
;LENGTH: 25
5189020-1

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY    1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
     |: | :| ||||| 
Db    1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 70
5189020-2
;Patent No. 5189020
;APPLICANT: Miljanich, George P.;Bitner, Robert S.;Bowersox, Stephen S.;Fox, James A.;Valentino, Karen L.;Yamashiro, Donald H.;Tsubokawa, Makoto
;TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING OMEGA CONOTOXIN PEPTIDES
;NUMBER OF SEQUENCES: 29
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/561,766
;FILING DATE: 02-AUG-1990
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 440,094
;FILING DATE: 22-NOV-1989
;SEQ ID NO:2:
;LENGTH: 25
5189020-2

Query Match      34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY    1 CRXNQKCFQHLLDDCCSRKNRPNKC 26
     |: | :| ||||| 
Db    1 CKKGASCHRTSYDCTGSCNR-GKC 25


RESULT 71
5424218-2
;Patent No. 5424218
;APPLICANT: MILJANICH, GEORGE P.;BITNER, ROBERT S.;BOWERSOX, STEPHEN S.;FOX, JAMES A.;VALENTINO, KAREN L.;YAMASHIRO, DONALD H.
;TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
;NUMBER OF SEQUENCES: 21
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/147,714
;FILING DATE: 04-NOV-1993
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 855,269
;FILING DATE: 23-MAR-1992
;APPLICATION NUMBER: 561,766
;FILING DATE: 02-AUG-1990
;APPLICATION NUMBER: 440,094
```

```
; APPLICANT: MILJANICH, GEORGE P.;BITNER, ROBERT S.;BOWERSOX,
; STEPHEN S.;FOX, JAMES A.;VALENTINO, KAFEN L.;YAMASHIRO,DONALD H.
; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,714
; FILING DATE: 04-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 855,269
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: 561,766
; FILING DATE: 02-AUG-1990
; APPLICATION NUMBER: 440,094
; FILING DATE: 22-NOV-1989
; SEQ ID NO:2:
; LENGTH: 25
5424218-2

Query Match          34.5%; Score 55.5; DB 6; Length 25;
Best Local Similarity 38.5%; Pred. No. 3.6;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 1 CRXKQKCFQHLDDCCSRKCNFKNC 25
   | : : : : : | : : : : : | : : : : : | : : : : : |
Db 1 CKGKGASCHRTSYDCCGTGCNCR-GKC 25

RESULT 75
US-07-689-693B-1
; Sequence 1, Application US/07689693B
; Patent No. 5231011
; GENERAL INFORMATION:
; APPLICANT: David Hillyard
; APPLICANT: Baldomero M. Olivera
; TITLE OF INVENTION: Segregated Folding Determinants
; TITLE OF INVENTION: for Small Disulfide-Rich Peptides
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5231011th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: Compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/689,693B
; FILING DATE: 19910418
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: 9925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Prepropeptide sequence for four-loop
; NAME/KEY: MVIIb Omega conotoxin from Conus magus.
; IDENTIFICATION METHOD: Libraries were created
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; IDENTIFICATION METHOD: using oligo-dT primed pUC13 vector
US-07-689-693B-1

Query Match          34.5%; Score 55.5; DB 1; Length 71;
Best Local Similarity 38.5%; Pred. No. 9;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

Qy 1 CRXKQKCFQHLDDCCSRKCNFKNC 26
   | : : : : : | : : : : : | : : : : : | : : : : : |
Db 46 CKGKGASCHRTSYDCCGTGCNCR-GKC 70

RESULT 76
US-08-937-236-3
; Sequence 3, Application US/08937236
; Patent No. 6187310
; GENERAL INFORMATION:
; APPLICANT: MANN, BARBARA J.
; APPLICANT: PETRI, WILLIAM A.
; APPLICANT: DODSON, JAMES M.
; TITLE OF INVENTION: RECOMBINANT ENTAMOEBA HISTOLYTICA LECTIN
; TITLE OF INVENTION: SUBUNIT PEPTIDES AND REAGENTS SPECIFIC FOR MEMBERS OF THE
; TITLE OF INVENTION: 170 KD SUBUNIT MOLLIGENE FAMILY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE N.W., STE. 5500
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 200006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,236
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/569,214
; FILING DATE: 16 SEPTEMBER 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: 291482000622
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1276 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-236-3

Query Match          34.5%; Score 55.5; DB 3; Length 1276;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

Qy 1 CRXKQKCFQHLDDCCSRK--CNRFN-KCV 27
   | : : : : : | : : : : : | : : : : : | : : : : : |
Db 702 CSMGTDTIITYHDDCNRSKSCQGNFGKCI 731

RESULT 77
US-08-569-214-3
; Sequence 3, Application US/08569214
; Patent No. 6165469
; GENERAL INFORMATION:
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LENGTH: 1295 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-569-214-2

Query Match 34.5%; Score 55.5; DB 3; Length 1295;
 Best Local Similarity 40.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXKQCFQHLDDCCSRK--CNRFN-KCV 27
 Db 717 CSMGTDNIITYHDDCNRRKSCQCNFGKCI 746

RESULT 80

US-08-049-794-21
 ; Sequence 21, Application US/08049794
 ; Patent No. 5587454
 ; GENERAL INFORMATION:
 ; APPLICANT: JUSTICE, ALAN
 ; APPLICANT: SINGH, TEJINDER
 ; APPLICANT: GOHIL, KISHOR C
 ; APPLICANT: VALENTINO, KAREN L
 ; APPLICANT: MILJANICH, GEORGE P
 ; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
 ; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Law Offices of Peter Dehlinger
 ; STREET: 350 Cambridge Avenue, Suite 300
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/049,794
 FILING DATE: 19930415
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/814,759
 FILING DATE: 30-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Stratford, Carol A.
 REGISTRATION NUMBER: 34,444
 REFERENCE/DOCKET NUMBER: 5865-0009.30
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 324-0880
 TELEFAX: (415) 324-0960
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 7
 OTHER INFORMATION: /note= "where X is hydroxyproline"

US-08-049-794-21
 Query Match 34.2%; Score 55; DB 1; Length 26;
 Best Local Similarity 47.4%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
 Db 8 CRKTMVDCSGSGCGRRGKC 26

RESULT 81

US-08-496-847-21
 ; Sequence 21, Application US/08496847
 ; Patent No. 5795864
 ; GENERAL INFORMATION:
 ; APPLICANT: Amstutz, Gary A.
 ; APPLICANT: Bowersox, Stephen S.
 ; APPLICANT: Gohil, Kishorchandra
 ; APPLICANT: Adriaenssens, Peter I.
 ; APPLICANT: Kristipati, Ramasharma
 ; TITLE OF INVENTION: METHODS AND
 ; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Avenue, Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94306-1546
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/496,847
 ; FILING DATE: 27-JUN-1995
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stratford, Carol A.
 ; REGISTRATION NUMBER: 34,444
 ; REFERENCE/DOCKET NUMBER: 5865-0009.31
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-324-0880
 ; TELEFAX: 650-324-0960
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 26 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 7
 ; OTHER INFORMATION: /note= "where X is hydroxyproline"

US-08-496-847-21
 Query Match 34.2%; Score 55; DB 1; Length 26;
 Best Local Similarity 47.4%; Pred. No. 4.3;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
 Db 8 CRKTMVDCSGSGCGRRGKC 26

RESULT 82

US-08-742-774-21
 ; Sequence 21, Application US/08742774
 ; Patent No. 5824645
 ; GENERAL INFORMATION:
 ; APPLICANT: JUSTICE, ALAN
 ; APPLICANT: SINGH, TEJINDER
 ; APPLICANT: GOHIL, KISHOR C

```

; APPLICANT: VALENTINO, KAREN L.
; APPLICANT: MILJANTICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/742,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/675,354
; FILING DATE: 03-JUL-1996
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US/07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-742-774-21

```

```

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 8 CFQHLDDCCSKNKNKNC 26
Db 8 CRKTYDCCSGCGRRGKC 26

```

RESULT 83

```

US-08-675-354-21
; Sequence 21, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANTICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/675,354
; FILING DATE: 03-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-APR-15
; APPLICATION NUMBER: US/07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-675-354-21

```

```

Query Match 34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 8 CFQHLDDCCSKNKNKNC 26
Db 8 CRKTYDCCSGCGRRGKC 26

```

RESULT 84

```

US-08-965-918-21
; Sequence 21, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; TITLE OF INVENTION: PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-08-965-918-21

```

```

Query Match      34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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```

Qy 8 CFQHLDDCCSRKCNRFNKC 26
Db 8 CRKTYDCCSGCGRRGKC 26

```

```

RESULT 85
US-09-138-439-21
; Sequence 21, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
US-09-138-439-21

```

```

Query Match      34.2%; Score 55; DB 2; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy 8 CFQHLDDCCSRKCNRFNKC 26
Db 8 CRKTYDCCSGCGRRGKC 26

```

```

RESULT 86
US-08-613-400A-21
; Sequence 21, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.
; TITLE OF INVENTION: IMPROVED EPIDURAL
; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/613,400A
; FILING DATE: 08-MAR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

; MOLECULE TYPE: 'protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 1
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-08-613-400A-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
| : ||||| ||
Db 8 CRKTYDCCSGCGRRGKC 26

RESULT 87
US-09-298-017-21
; Sequence 21, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/298,017
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/049,794
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-298-017-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
| : ||||| ||
Db 8 CRKTYDCCSGCGRRGKC 26

RESULT 88
US-09-392-979A-21
; Sequence 21, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-231, FIGURE 2
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 7
; OTHER INFORMATION: /note= "where X is hydroxyproline"
; US-09-392-979A-21

Query Match 34.2%; Score 55; DB 3; Length 26;
Best Local Similarity 47.4%; Pred. No. 4.3;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFNKC 26
| : ||||| ||
Db 8 CRKTYDCCSGCGRRGKC 26

```
RESULT 89
US-09-949-016-9481
; Sequence 9481, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9481
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9481

Query Match 34.2%; Score 55; DB 4; Length 473;
Best Local Similarity 44.0%; Pred. No. 54;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

Qy 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
Db 89 RAWHVQVQ-----CCECKCNLTKEC 109

RESULT 90
US-09-641-612-2
; Sequence 2, Application US/09641612
; Patent No. 6703221
; GENERAL INFORMATION:
; APPLICANT: Vivien Chan et al.
; TITLE OF INVENTION: NOTCH RECEPTOR LIGANDS AND USES THEREOF
; FILE REFERENCE: PPO-1602.002 / 200130.458
; CURRENT APPLICATION NUMBER: US/09/641,612
; CURRENT FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 583
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-641-612-2

Query Match 34.2%; Score 55; DB 4; Length 583;
Best Local Similarity 37.9%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CR--IXNQKCFQHLDDCCSRKCNRFNKC 27
Db 375 CRAGFAGPRCEHLDLDDCAGACANGTCV 403

RESULT 91
US-07-789-913-1
; Sequence 1, Application US/077899913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
```

```
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-111
US-07-789-913-1

Query Match 33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRFNKC 26
Db 1 CKGKGAQCSRLMYDCTGSC-RSGKC 25

RESULT 92
US-07-789-913-9
; Sequence 9, Application US/077899913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; TITLE OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
```



```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: MVIIA/SNX-111, FIGURE 1
; US-08-049-794-1
;
Query Match 33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels

QY 1 CRXNOKCFQHLDCCSKRCNRFNKC 26
   | : ||| : |||
Db 1 CKKGAKCSRLMYDCTGSC-RSGKC 25

RESULT 94
US-08-049-794-9
; Sequence 9, Application US/08049794
; Patent No. 5587454
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: AMINO ACID

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
US-08-049-794-9

Query Match      33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
| : : : : : : : : : : : :
Db 1 CKGAGAKCSRLMYDCTGSC-RSGKC 25

RESULT 95
US-08-496-847-1
; Sequence 1, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELEPHONE: 650-324-0960
; TELEFAX: 650-324-0880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: VIIIA/SNX-111, FIGURE 1
US-08-496-847-1

Query Match      33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
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Db 1 CKGAGAKCSRLMYDCTGSC-RSGKC 25

RESULT 96
US-08-496-847-1
; Sequence 1, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELEPHONE: 650-324-0960
; TELEFAX: 650-324-0880
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: VIIIA/SNX-111, FIGURE 1
US-08-496-847-1

Query Match      33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
| : : : : : : : : : : : :
Db 1 CKGAGAKCSRLMYDCTGSC-RSGKC 25

RESULT 97
US-08-496-847-9
; Sequence 9, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELEPHONE: 650-324-0960
; TELEFAX: 650-324-0880
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: SNX-190, FIGURE 2
US-08-496-847-9

Query Match      33.9%; Score 54.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNFNKC 26
| : : : : : : : : : : : :
Db 1 CKGAGAKCSRLMYDCTGSC-RSGKC 25

RESULT 97
US-08-742-774-1
; Sequence 1, Application US/08742774
; Patent No. 5824645
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REGISTER/DOCKET NUMBER: 5865-0009.30

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: MVIIA/ST
US-08-675-354-1

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Query Match      . 33.9%; Score 54.5; DB 2; Length 35;  
Best Local Similarity 38.5%; Pred.Nc.4.7;  
Matches 10; Conservative 5; Mismatches 10; Indels  
  
Qy   1 CRXNQKCFQHLDCCSRKCNRFNK 26  
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Db   1 CKGGAKCSRIMYDCCTGTSC-RSGKK 25
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RESULT 100
US-08-675-354-9
; Sequence 9, Application US/08675354
; Patent No. 5859186
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:

US-08-675-354-9

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Query Match          33.9%;   Score 54.5;   DB 2;   Length 25;
Best Local Similarity 38.5%;   Pred. No. 4.7;
Matches 10;   Conservative 5;   Mismatches 10;   Indels 1;   Gaps 1;

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db 1 KGAGAKCSRLMYDCTGSC-RSGKC 25

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Search completed: April 18, 2005, 20:39:52
Job time : 31.5 secs

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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:29:42 ; Search time 91.5 Seconds
(without alignments)

98.077 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161

Sequence: 1 CR1XNQKCFQHLDDCCSRKCNRFNKC 27

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Searched: 1421835 seqs, 332370693 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	161	100.0	27	15	US-10-352-254-24
2	161	100.0	27	15	US-10-627-685-24
3	158	98.1	27	15	US-10-352-254-9
4	158	98.1	27	15	US-10-352-254-12
5	158	98.1	27	15	US-10-352-254-18
6	158	98.1	27	15	US-10-627-685-9
7	158	98.1	27	15	US-10-627-685-12
8	158	98.1	27	15	US-10-627-685-18
9	157	97.5	27	15	US-10-352-254-13
10	157	97.5	27	15	US-10-352-254-23
11	157	97.5	27	15	US-10-627-685-13
12	157	97.5	27	15	US-10-627-685-23
13	156	96.9	27	15	US-10-352-254-4

14	156	96.9	27	15	US-10-352-254-20	Sequence 20, Appl
15	156	96.9	27	15	US-10-627-685-4	Sequence 4, Appl
16	156	96.9	27	15	US-10-627-685-20	Sequence 20, Appl
17	155	96.3	27	15	US-10-352-254-2	Sequence 2, Appl
18	155	96.3	27	15	US-10-352-254-3	Sequence 3, Appl
19	155	96.3	27	15	US-10-352-254-5	Sequence 5, Appl
20	155	96.3	27	15	US-10-352-254-6	Sequence 6, Appl
21	155	96.3	27	15	US-10-352-254-8	Sequence 8, Appl
22	155	96.3	27	15	US-10-352-254-10	Sequence 10, Appl
23	155	96.3	27	15	US-10-352-254-11	Sequence 11, Appl
24	155	96.3	27	15	US-10-352-254-16	Sequence 16, Appl
25	155	96.3	27	15	US-10-352-254-22	Sequence 22, Appl
26	155	96.3	27	15	US-10-627-685-2	Sequence 2, Appl
27	155	96.3	27	15	US-10-627-685-3	Sequence 3, Appl
28	155	96.3	27	15	US-10-627-685-5	Sequence 5, Appl
29	155	96.3	27	15	US-10-627-685-6	Sequence 6, Appl
30	155	96.3	27	15	US-10-627-685-8	Sequence 8, Appl
31	155	96.3	27	15	US-10-627-685-10	Sequence 10, Appl
32	155	96.3	27	15	US-10-627-685-11	Sequence 11, Appl
33	155	96.3	27	15	US-10-627-685-16	Sequence 16, Appl
34	155	96.3	27	15	US-10-627-685-22	Sequence 22, Appl
35	153	95.0	27	15	US-10-352-254-7	Sequence 7, Appl
36	153	95.0	27	15	US-10-352-254-15	Sequence 15, Appl
37	153	95.0	27	15	US-10-352-254-17	Sequence 17, Appl
38	153	95.0	27	15	US-10-352-254-19	Sequence 19, Appl
39	153	95.0	27	15	US-10-352-254-21	Sequence 21, Appl
40	153	95.0	27	15	US-10-352-254-25	Sequence 25, Appl
41	153	95.0	27	15	US-10-627-685-7	Sequence 7, Appl
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43	153	95.0	27	15	US-10-627-685-17	Sequence 17, Appl
44	153	95.0	27	15	US-10-627-685-19	Sequence 19, Appl
45	153	95.0	27	15	US-10-627-685-21	Sequence 21, Appl
46	153	95.0	27	15	US-10-627-685-25	Sequence 25, Appl
47	151	93.8	27	15	US-10-352-254-14	Sequence 14, Appl
48	151	93.8	27	15	US-10-627-685-14	Sequence 14, Appl
49	78.5	48.8	27	16	US-09-910-082A-354	Sequence 354, App
50	78.5	48.8	27	16	US-10-765-926-354	Sequence 354, App
51	78.5	48.8	72	10	US-09-910-082A-130	Sequence 130, App
52	78.5	48.8	72	16	US-10-765-926-130	Sequence 130, App
53	74	46.0	26	10	US-09-910-082A-395	Sequence 395, App
54	74	46.0	26	16	US-10-765-926-395	Sequence 395, App
55	74	46.0	30	10	US-09-910-082A-257	Sequence 257, App
56	74	46.0	30	16	US-10-765-926-257	Sequence 257, App
57	73	45.3	72	10	US-09-910-082A-217	Sequence 217, App
58	73	45.3	72	16	US-10-765-926-217	Sequence 217, App
59	71	44.1	27	16	US-09-910-082A-384	Sequence 384, App
60	71	44.1	27	16	US-10-765-926-384	Sequence 384, App
61	71	44.1	72	10	US-09-910-082A-223	Sequence 223, App
62	71	44.1	72	16	US-10-765-926-223	Sequence 223, App
63	67	41.6	26	10	US-09-910-082A-258	Sequence 258, App
64	67	41.6	26	16	US-10-765-926-258	Sequence 258, App
65	64	39.8	26	10	US-09-910-082A-268	Sequence 268, App
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68	64	39.8	27	16	US-10-765-926-218	Sequence 218, App
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73	63.5	39.4	73	10	US-09-910-082A-94	Sequence 94, Appl
74	63.5	39.4	73	16	US-10-765-926-94	Sequence 94, Appl
75	62.5	38.8	36	9	US-09-894-882-369	Sequence 369, App
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77	62	38.5	27	10	US-09-910-082A-224	Sequence 224, App
78	62	38.5	27	16	US-10-765-926-224	Sequence 224, App
79	62	38.5	76	9	US-09-749-637A-207	Sequence 207, App
80	61.5	38.2	27	10	US-09-910-082A-131	Sequence 131, App
81	61.5	38.2	27	16	US-10-765-926-131	Sequence 131, App
82	61	37.9	27	10	US-09-910-082A-359	Sequence 359, App
83	61	37.9	27	16	US-10-765-926-359	Sequence 359, App
84	61	37.9	74	10	US-09-910-082A-5	Sequence 5, Appl
85	61	37.9	74	16	US-10-765-926-5	Sequence 5, Appl
86	59.5	37.0	27	10	US-09-910-082A-236	Sequence 236, App

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RESULT 4
US-10-352-254-12
; Sequence 12, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related
; FILE REFERENCE: 2314-254
Conotoxins

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; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-13

Query Match
Best Local Similarity 97.5%; Score 157; DB 15; Length 27;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 1 CQIXNQKCFQHLDDCCSRKCNRFNKC 27

RESULT 12
US-10-627-685-23
; Sequence 23, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Leyer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
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; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23

Query Match
Best Local Similarity 97.5%; Score 157; DB 15; Length 27;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26

RESULT 13
US-10-352-254-4
; Sequence 4, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen

; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-23

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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
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RESULT 14
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; Sequence 20, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-20

Query Match
Best Local Similarity 96.9%; Score 156; DB 15; Length 27;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 1 CRAXNQKCFQHLDDCCSRKCNRFNKC 27

RESULT 15
US-10-627-685-4
; Sequence 4, Application US/10627685
```

```

; Publication No. US20040092447A1
;
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
;
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIIA
;
; FILE REFERENCE: Kappa-PVIIA
;
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
;
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
;
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
;
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
;
; NUMBER OF SEQ ID NOS: 25
;
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 4
;
; LENGTH: 27
;
; TYPE: RPT
;
; ORGANISM: Conus purpurascens
;
; FEATURE:
;
; NAME/KEY: PEPTIDE
;
; LOCATION: (1)..(27)
;
; OTHER INFORMATION: Xaa is Hyp
;
; US-10-627-685-4

```

```

Query Match          96.9%;   Score 156;   DB 15;   Length 27;
Best Local Similarity 96.3%;   Pred. No. 4.9e-12;
Matches 26;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  CRXNQKCFQHLDDCCSRKCNRFNKCV  27
Db   1  CRXNQKCFQHLDDCCSRKCNRFNKCV  27

```

```

RESULT 16
US/10-627-685-20
; Sequence 20, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-20

```

```

Query Match      96.9%; Score 156; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 4.9e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27
Db 1 CRIXNQKCFQHLDDCCSRKCNRFNKCV 27

```

```

RESULT 17
US-10-352-254-2
; Sequence 2, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-2

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```

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRENKCV 27
Db 1 CRXNQKCFQHLDDCCSAKCNRENKCV 27

```

```

RESULT 18
US-10-352-254-3
; Sequence 3, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatenIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens

```

```
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-3

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27
Db 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27

RESULT 19
US-10-352-254-5
; Sequence 5, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-5

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27
Db 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27

RESULT 20
US-10-352-254-6
; Sequence 6, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
```

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-6

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27
Db 1 CAIXNKCFOHLDCCSRKCNRFNKCVCV 27

RESULT 21
US-10-352-254-8
; Sequence 8, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-8

Query Match          96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27
Db 1 CRXNKCFOHLDCCSRKCNRFNKCVCV 27

RESULT 22
US-10-352-254-10
; Sequence 10, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
```

; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-10

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 23

US-10-352-254-11
; Sequence 11, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-11

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 24

US-10-352-254-16
; Sequence 16, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.

; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-16

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 25

US-10-352-254-22
; Sequence 22, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-22

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQACFQHLDDCCSRKCNRFNKCVCV 27

RESULT 26

US-10-627-685-2
; Sequence 2, Application US/10627685
; Publication No. US20040092447A1

; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-6

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CAIXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 30

US-10-627-685-8
; Sequence 8, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-8

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNACV 27

RESULT 31

US-10-627-685-10
; Sequence 10, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.

; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-10

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 32

US-10-627-685-11
; Sequence 11, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornelli-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp

US-10-627-685-11

Query Match 96.3%; Score 155; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 6.5e-12;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

RESULT 34
US-10-627-685-22
; Sequence 22, Application US/10627685
; Publication NO. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22

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RESULT 36
US-10-352-254-15
; Sequence 15, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28

; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-15

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 37

US-10-352-254-17
; Sequence 17, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 38

US-10-352-254-19
; Sequence 19, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael

; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-19

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 39

US-10-352-254-21
; Sequence 21, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Pemberton-Goodman, Karen
; APPLICANT: Jones, Robert M.
; APPLICANT: Temple, Davis
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
; FILE REFERENCE: 2314-254
; CURRENT APPLICATION NUMBER: US/10/352,254
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/352,219
; PRIOR FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-352-254-21

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27
Db 1 CRXNQKCFQHLDDCCSRKCNRFNKCVCV 27

RESULT 40

US-10-352-254-25
; Sequence 25, Application US/10352254
; Publication No. US20030224343A1
; GENERAL INFORMATION:
; APPLICANT: Cognetix, Inc.

APPLICANT: University of Utah Research Foundation
APPLICANT: Pemberton-Goodman, Karen
APPLICANT: Jones, Robert M.
APPLICANT: Temple, Davis
APPLICANT: McIntosh, J. Michael
APPLICANT: Olivera, Baldomero M.
TITLE OF INVENTION: Kappa-PVIIA-Related Conotoxins as Organ Protectants
FILE REFERENCE: 2314-254
CURRENT APPLICATION NUMBER: US/10/352,254
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/352,219
PRIOR FILING DATE: 2002-01-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-352-254-25

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 41
US-10-627-685-7
Sequence 7, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-7

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 42
US-10-627-685-15
Sequence 15, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-15

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

RESULT 43
US-10-627-685-17
Sequence 17, Application US/10627685
Publication No. US20040092447A1
GENERAL INFORMATION:
APPLICANT: Cornell-Bell, Ann H.
APPLICANT: Pemberton, Karen E.
APPLICANT: Temple Jr., Davis L.
APPLICANT: Layer, Richard T.
APPLICANT: McCabe, R. Tyler
APPLICANT: Jones, Robert M.
APPLICANT: Cognetix, Inc.
TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
FILE REFERENCE: Kappa-PVIIA
CURRENT APPLICATION NUMBER: US/10/627,685
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/666,837
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/219,438
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/155,135
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 27
TYPE: PRT
ORGANISM: Conus purpurascens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(27)
OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27
|||||
DB 1 CRXNQKCFQHLDDCCSRKCNRFNKCV 27

; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-17

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 44

US-10-627-685-19
; Sequence 19, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-19

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 45

US-10-627-685-21
; Sequence 21, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA

; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-21

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 46

US-10-627-685-25
; Sequence 25, Application US/10627685
; Publication No. US20040092447A1
; GENERAL INFORMATION:
; APPLICANT: Cornell-Bell, Ann H.
; APPLICANT: Pemberton, Karen E.
; APPLICANT: Temple Jr., Davis L.
; APPLICANT: Layer, Richard T.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Jones, Robert M.
; APPLICANT: Cognetix, Inc.
; TITLE OF INVENTION: Uses of Kappa-Conotoxin PVIIA
; FILE REFERENCE: Kappa-PVIIA
; CURRENT APPLICATION NUMBER: US/10/627,685
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/666,837
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/219,438
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/155,135
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa is Hyp
US-10-627-685-25

Query Match 95.0%; Score 153; DB 15; Length 27;
Best Local Similarity 96.3%; Pred. No. 1.1e-11;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||
DB 1 CRXNKKCFQHLDDCCSRKCNRFNKCVCV 27
|||||

RESULT 47


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; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 354
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-354

Query Match
  48.8%; Score 78.5; DB 16; Length 27;
Best Local Similarity 46.2%; Pred. No. 0.011;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | | | | : | |
Db 2 CKPKGRKCFPHQKDCCKNTCTR-SKC 26

RESULT 51
US-09-910-082A-130
; Sequence 130, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; CURRENT APPLICATION NUMBER: US/09/910,082A
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus ermineus
US-09-910-082A-130

Query Match
  48.8%; Score 78.5; DB 10; Length 72;
Best Local Similarity 46.2%; Pred. No. 0.025;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | | | | : | |
Db 47 CKPKGRKCFPHQKDCCKNTCTR-SKC 71

RESULT 52
US-10-765-926-130
; Sequence 130, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
```

```
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 130
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus ermineus
US-10-765-926-130

Query Match
  48.8%; Score 78.5; DB 16; Length 72;
Best Local Similarity 46.2%; Pred. No. 0.025;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | | | | : | |
Db 47 CKPKGRKCFPHQKDCCKNTCTR-SKC 71

RESULT 53
US-09-910-082A-395
; Sequence 395, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 395
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-910-082A-395

Query Match
  46.0%; Score 74; DB 10; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.037;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | : : : : | | | | : | |
Db 1 CKLKQSCRRRTMYDCCSGCGRRGKC 26

RESULT 54
US-10-765-926-395
; Sequence 395, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
```

```

; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 395
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
US-10-765-926-395

```

```

Query Match      46.0%; Score 74; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.037;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | | | | | | | | | | | | | |
DB 1 CLKGQSCRTMYDCCSGCGRRGKC 26

```

```

RESULT 55
US-09-910-082A-257
; Sequence 257, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 257
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striatus
US-09-910-082A-257

```

```

Query Match      46.0%; Score 74; DB 10; Length 30;
Best Local Similarity 42.3%; Pred. No. 0.042;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | | | | | | | | | | | | | |
DB 4 CLKGQSCRTMYDCCSGCGRRGKC 29

```

```

RESULT 56
US-10-765-926-257
; Sequence 257, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 257
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Conus striatus
US-10-765-926-257

```

```

Query Match      46.0%; Score 74; DB 16; Length 30;
Best Local Similarity 42.3%; Pred. No. 0.042;
Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

```

```

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
   | | | | | | | | | | | | | |
DB 4 CLKGQSCRTMYDCCSGCGRRGKC 29

```

```

RESULT 57
US-09-910-082A-217
; Sequence 217, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens

```

US-09-910-082A-217

Query Match 45.3%; Score 73; DB 10; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : : : : |
DB 47 CKTPGRKCFPHQKDCGRAC 66

RESULT 58

US-10-765-926-217
; Sequence 217, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 217
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-217

Query Match 45.3%; Score 73; DB 16; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : : : : |
DB 47 CKTPGRKCFPHQKDCGRAC 66

RESULT 59

US-09-910-082A-384
; Sequence 384, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 384
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-910-082A-384

Query Match 44.1%; Score 71; DB 10; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.087;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : : : : |
DB 2 CKKTGRKCFPHQKDCGRAC 21

RESULT 60

US-10-765-926-384
; Sequence 384, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 384
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-10-765-926-384

Query Match 44.1%; Score 71; DB 16; Length 27;
Best Local Similarity 50.0%; Pred. No. 0.087;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
| : : : : : |
DB 2 CKKTGRKCFPHQKDCGRAC 21

RESULT 61

US-09-910-082A-223
; Sequence 223, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 223
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Conus purpurascens
US-09-910-082A-223

Query Match 44.1%; Score 71; DB 10; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKC 20
| : : ||| | ||| |
DB 47 CKXGKCFPHQKCCGRAC 66

RESULT 62

US-10-765-926-223
; Sequence 223, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon

; APPLICANT: Jacobsen, Richard

; APPLICANT: Jones, Robert M.

; APPLICANT: Cartier, G. Edward

; TITLE OF INVENTION: Omega-Conopeptides

; FILE REFERENCE: 2314-241

; CURRENT APPLICATION NUMBER: US/10/765,926

; CURRENT FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US 09/910,082

; PRIOR FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 223

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Conus purpurascens

US-10-765-926-223

Query Match 44.1%; Score 71; DB 16; Length 72;
Best Local Similarity 50.0%; Pred. No. 0.2;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKC 20
| : : ||| | ||| |
DB 47 CKXGKCFPHQKCCGRAC 66

RESULT 63

US-09-910-082A-258

; Sequence 258, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward

; TITLE OF INVENTION: Omega-Conopeptides

; FILE REFERENCE: 2314-241

; CURRENT APPLICATION NUMBER: US/09/910,082A

; CURRENT FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 258

; LENGTH: 26

; TYPE: PRT

; ORGANISM: Conus striatus

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(26)

; OTHER INFORMATION: Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O

; OTHER INFORMATION: -sulpho-Tyr or O-phospho-Tyr

US-09-910-082A-258

Query Match 41.6%; Score 67; DB 10; Length 26;

Best Local Similarity 42.3%; Pred. No. 0.26;

Matches 11; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRXNKKCFQHLDDCCSRKCNRFNC 26
| : : ||| | ||| |
DB 1 CKXGQSCRRRTMXDCSCSGSGRRGKC 26

RESULT 64

US-10-765-926-258

; Sequence 258, Application US/10765926

; Publication No. US20040132663A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J. Michael

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Shon, Ki-Joon

; APPLICANT: Jacobsen, Richard

; APPLICANT: Jones, Robert M.

; APPLICANT: Cartier, G. Edward

; TITLE OF INVENTION: Omega-Conopeptides

; FILE REFERENCE: 2314-241

; CURRENT APPLICATION NUMBER: US/10/765,926

; CURRENT FILING DATE: 2004-01-29

; PRIOR APPLICATION NUMBER: US 09/910,082

; PRIOR FILING DATE: 2001-07-23

; PRIOR APPLICATION NUMBER: US 60/219,616

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/265,888

; PRIOR FILING DATE: 2001-02-05

; NUMBER OF SEQ ID NOS: 413

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 258

; LENGTH: 26

; TYPE: PRT

```

; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 268
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Conus striatus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(26)
; OTHER INFORMATION: xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr
; OTHER INFORMATION: di-iodo-Tyr, O -sulpho-Tyr or O-phospho-Tyr
US-09-910-082A-268

Query Match          39.8%; Score 64; DB 16; Length 26;
Best Local Similarity 42.3%; Pred. No. 0.59;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps

QY 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
   |:::|::|::|::|::|::|::|::|
DB 1 CKLKGQSCRKTSXDCSGSCGRSGKC 26

RESULT 67
US-09-910-082A-218
; Sequence 218, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 218
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: xaa at residue 1, 5, 11 and 27 is Pro or Hyp
US-09-910-082A-218

Query Match          39.8%; Score 64; DB 10; Length 27;
Best Local Similarity 55.0%; Pred. No. 0.61;

```


APPLICANT: GONZALEZ, ROBERT L.
 APPLICANT: Cartier, G. Edward
 TITLE OF INVENTION: Omega-Conopeptides
 FILE REFERENCE: 2314-241
 CURRENT APPLICATION NUMBER: US/10/765,9
 CURRENT FILING DATE: 2004-01-29
 PRIOR APPLICATION NUMBER: US 09/910,082
 PRIOR FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: US 6/219,616

US-09-910-082A-350
: Sequence 350, Application US/09910082A

```

; Publication No. US20030119731A1
;
; GENERAL INFORMATION:
;
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
;
; TITLE OF INVENTION: Omega-Conopeptides
;
; FILE REFERENCE: 2314-241
;
; CURRENT APPLICATION NUMBER: US/09/910,082A
;
; CURRENT FILING DATE: 2001-07-23
;
; PRIOR APPLICATION NUMBER: US 60/219,616
;
; PRIOR FILING DATE: 2000-07-21
;
; PRIOR APPLICATION NUMBER: US 60/265,888
;
; PRIOR FILING DATE: 2001-02-05
;
; NUMBER OF SEQ ID NOS: 413
;
; SOFTWARE: PatentIn version 3.0
;
; SEQ ID NO 350
;
; LENGTH: 27
;
; TYPE: PRT
;
; ORGANISM: Conus circumcissus
;
; US-09-910-082A-150

```

Query Match 39.4%; Score 63.5; DB 10; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

Qy	1	CRIXNQKCFQHLDDCCSRKCNRFN-KC	26
		: : : : : : : :	
Dd	1	CKSKGAKCRLMYDCCSGCSRYSGRC	27

```

RESULT 72
US-10-765-926-350
; Sequence 350, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10765,926
; PRIOR FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 350
; LENGTH: 27
; TYPE: PR1
; ORGANISM: Conus circumciscus
US-10-765-926-350

```

Query Match 39.4%; Score 63.5; DB 16; Length 27;
Best Local Similarity 37.0%; Pred. No. 0.7;
Matches 10; Conservative 8; Mismatches 8; Indels

Qy	1	CRIXNQKCFQHLDDCCSRKCNREN-KC	26
		: : : : : : :	
Db	1	CKSKGAKCSRLMYDCCSGSCSYSGRC	27

```

RESULT 73
US-09-910-082A-94
; Sequence 94, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus circumcissus
US-09-910-082A-94

```

```

Query March          39.4%; Score 63.5; DB 10; Length 73;
Best Local Similarity 37.0%; Pred. No. 1.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY      1 CRXNOKCFQHLDDCCSRKCNRFN-KC 26
      | : | : | | | | | : : : |
DB      46 CKSGKAKCRLMYDCCGSCSYSGRC 72

```

RESULT 74
US-10-765-926-94
Sequence 94, Application US/10765926
Publication No. US20040132663A1

RESULT 74
 US-10-765-926-94
 Sequence 94, Application US/10765926
 Publication No. US20040132663A1
 GENERAL INFORMATION:
 APPLICANT: University of Utah Research Foundation
 APPLICANT: Cognetix, Inc.
 APPLICANT: Olivera, Baldomero M.
 APPLICANT: McIntosh, J. Michael
 APPLICANT: Watkins, Maren
 APPLICANT: Garrett, James E.
 APPLICANT: Shon, Ki-Joon
 APPLICANT: Jacobsen, Richard
 APPLICANT: Jones, Robert M.
 APPLICANT: Cartier, G. Edward
 TITLE OF INVENTION: Omega-Conopeptides
 FILE REFERENCE: 2314-241
 CURRENT APPLICATION NUMBER: US/10/765,926
 CURRENT FILING DATE: 2004-01-29
 PRIOR APPLICATION NUMBER: US 09/910,082
 PRIOR FILING DATE: 2001-07-23
 PRIOR APPLICATION NUMBER: US 60/219,616
 PRIOR FILING DATE: 2000-07-21
 PRIOR APPLICATION NUMBER: US 60/265,888
 PRIOR FILING DATE: 2001-02-05
 NUMBER OF SEQ ID NOS: 413
 SOFTWARE: Patent in version 3.0

```
; SEQ ID NO 94
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus circumcinctus
US-10-765-926-94

Query Match      39.4%; Score 63.5; DB 16; Length 73;
Best Local Similarity 37.0%; Pred. No. 1.7;
Matches 10; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFN-KC 26
Db 46 CKSKGAKCSRLMYDCCSGSCSYSGRC 72

RESULT 75
US-09-894-882-369
; Sequence 369, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma C.
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 369
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-369

Query Match      38.8%; Score 62.5; DB 9; Length 36;
Best Local Similarity 40.7%; Pred. No. 1.2;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 2 CLSLGQRCERH-SDCCGYLCCFYDKCV 27

RESULT 76
US-09-894-882-167
; Sequence 167, Application US/09894882
; Patent No. US20020102607A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Walker, Craig S.
; APPLICANT: Shetty, Reshma
; APPLICANT: Jimenez, Elsie C.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
```

```
; APPLICANT: Watkins, Maren
; APPLICANT: Jones, Robert M.
; APPLICANT: Shen, Greg S.
; TITLE OF INVENTION: I-Superfamily Conotoxins
; FILE REFERENCE: 2314-238
; CURRENT APPLICATION NUMBER: US/09/894,882
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/243,410
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/246,581
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/247,714
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/264,256
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 167
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Conus betulinus
US-09-894-882-167

Query Match      38.8%; Score 62.5; DB 9; Length 73;
Best Local Similarity 40.7%; Pred. No. 2.2;
Matches 11; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 39 CLSLGQRCERH-SDCCGYLCCFYDKCV 64

RESULT 77
US-09-910-082A-224
; Sequence 224, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 224
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus purpurascens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(27)
; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
US-09-910-082A-224

Query Match      38.5%; Score 62; DB 10; Length 27;
Best Local Similarity 50.0%; Pred. No. 1.1;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

QY 1 CRXNOKCFQHLDDCCSRKC 20
 | : : ||| | ||| | ||| |
 Db 2 CKTKGRKCFXHQKDCGRAC 21

RESULT 78

US-10-765-926-224
 ; Sequence 224, Application US/10765926
 ; Publication No. US20040132663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J. Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Shon, Ki-Joon
 ; APPLICANT: Jacobsen, Richard
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Cartier, G. Edward
 ; TITLE OF INVENTION: Omega-Conopeptides
 ; FILE REFERENCE: 2314-241
 ; CURRENT APPLICATION NUMBER: US/10/765,926
 ; PRIOR FILING DATE: 2004-01-29
 ; PRIOR APPLICATION NUMBER: US 09/910,082
 ; PRIOR FILING DATE: 2001-07-23
 ; PRIOR APPLICATION NUMBER: US 60/219,616
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: US 60/265,888
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 224
 ; LENGTH: 27
 ; TYPE: PRT
 ; ORGANISM: Conus purpurascens
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)...(27)
 ; OTHER INFORMATION: Xaa at residue 1, 11 and 27 is Pro or Hyp
 US-10-765-926-224

Query Match 38.5%; Score 62; DB 16; Length 27;
 Best Local Similarity 50.0%; Pred. No. 1.1;
 Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNOKCFQHLDDCCSRKC 20
 | : : ||| | ||| | ||| |
 Db 2 CKTKGRKCFXHQKDCGRAC 21

RESULT 79

US-09-749-637A-207
 ; Sequence 207, Application US/09749637A
 ; Patent No. US20020173449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: Cartier, G. Edward
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Hillyard, David R.
 ; APPLICANT: McIntosh, J. Michael
 ; APPLICANT: Layer, Richard T.
 ; APPLICANT: Jones, Robert M.
 ; TITLE OF INVENTION: O-Superfamily Conotoxin Peptides
 ; FILE REFERENCE: 2314-227
 ; CURRENT APPLICATION NUMBER: US/09/749,637A
 ; CURRENT FILING DATE: 2000-12-28
 ; PRIOR APPLICATION NUMBER: US 60/243,412
 ; PRIOR FILING DATE: 2000-10-27
 ; PRIOR APPLICATION NUMBER: US60/219,440
 ; PRIOR FILING DATE: 2000-07-20

; PRIOR APPLICATION NUMBER: US 60/214,263
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: US 60/173,754
 ; PRIOR FILING DATE: 1999-12-30
 ; NUMBER OF SEQ ID NOS: 409
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 207
 ; LENGTH: 76
 ; TYPE: PRT
 ; ORGANISM: Conus distans
 US-09-749-637A-207

Query Match 38.5%; Score 62; DB 9; Length 76;
 Best Local Similarity 39.3%; Pred. No. 2.6;
 Matches 11; Conservative 6; Mismatches 9; Indels 2; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRKCNRP-NKCV 27
 | : : ||| | ||| | ||| | ||| |
 Db 48 CNEAQEHCTQN-PDCCSCKNFVGRCL 74

RESULT 80

US-09-910-082A-131
 ; Sequence 131, Application US/09910082A
 ; Publication No. US20030119731A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.
 ; APPLICANT: McIntosh, J. Michael
 ; APPLICANT: Watkins, Maren
 ; APPLICANT: Garrett, James E.
 ; APPLICANT: Shon, Ki-Joon
 ; APPLICANT: Jacobsen, Richard
 ; APPLICANT: Jones, Robert M.
 ; APPLICANT: Cartier, G. Edward
 ; TITLE OF INVENTION: Omega-Conopeptides
 ; FILE REFERENCE: 2314-241
 ; CURRENT APPLICATION NUMBER: US/09/910,082A
 ; CURRENT FILING DATE: 2001-07-23
 ; PRIOR APPLICATION NUMBER: US 60/219,616
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: US 60/265,888
 ; PRIOR FILING DATE: 2001-02-05
 ; NUMBER OF SEQ ID NOS: 413
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 131
 ; LENGTH: 27
 ; TYPE: PRT
 ; ORGANISM: Conus ermineus
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)...(27)
 ; OTHER INFORMATION: Xaa at residue 1, 4, 11 and 27 is Pro or Hyp
 US-09-910-082A-131

Query Match 38.2%; Score 61.5; DB 10; Length 27;
 Best Local Similarity 47.8%; Pred. No. 1.2;
 Matches 11; Conservative 5; Mismatches 6; Indels 1; Gaps 1;

QY 4 XNOKCFQHLDDCCSRKCNRPNC 26
 | : : ||| | ||| | ||| | ||| |
 Db 5 KGRKCFXHQKDCNKTCTR-SKC 26

RESULT 81

US-10-765-926-131
 ; Sequence 131, Application US/10765926
 ; Publication No. US20040132663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Utah Research Foundation
 ; APPLICANT: Cognetix, Inc.
 ; APPLICANT: Olivera, Baldomero M.

Query Match 37.9%; Score 61; DB 10; Length 27;
Best Local Similarity 38.1%; Pred. No. 1.4;

```
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 74
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: unknown Conus species
US-09-910-082A-5

Query Match      37.9%; Score 61; DB 10; Length 74;
Best Local Similarity 38.1%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCN 21
   | : : : | | : : : | |
Db 47 CKPGRKCLNRKNECCSKFCN 67

RESULT 85
US-10-765-926-5
/ Sequence 5, Application US/10765926
/ Publication No. US20040132663A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ TITLE OF INVENTION: Omega-Conopeptides
/ FILE REFERENCE: 2314-241
/ CURRENT APPLICATION NUMBER: US/10/765,926
/ CURRENT FILING DATE: 2004-01-29
/ PRIOR APPLICATION NUMBER: US 09/910,082
/ PRIOR FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: US 60/219,616
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: US 60/265,888
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 5
/ LENGTH: 74
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: unknown Conus species
US-10-765-926-5

Query Match      37.9%; Score 61; DB 16; Length 74;
Best Local Similarity 38.1%; Pred. No. 3.4;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCN 21
   | : : : | | : : : | |
Db 47 CKPGRKCLNRKNECCSKFCN 67

RESULT 86
US-09-910-082A-236
/ Sequence 236, Application US/09910082A
/ Publication No. US20030119731A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ TITLE OF INVENTION: Omega-Conopeptides
/ FILE REFERENCE: 2314-241
/ CURRENT APPLICATION NUMBER: US/09/910,082A
/ CURRENT FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: US 60/219,616
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: US 60/265,888
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 390
/ LENGTH: 27
/ TYPE: PRT
/ ORGANISM: Conus rattus
US-09-910-082A-390

Query Match      37.0%; Score 59.5; DB 10; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCN 22
   | : : : | | : : : | |
Db 1 CNARNDGCSQH-SQCCSGSCNK 21

RESULT 87
US-09-910-082A-390
/ Sequence 390, Application US/09910082A
/ Publication No. US20030119731A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Olivera, Baldomero M.
/ APPLICANT: McIntosh, J. Michael
/ APPLICANT: Watkins, Maren
/ APPLICANT: Garrett, James E.
/ APPLICANT: Shon, Ki-Joon
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Cartier, G. Edward
/ APPLICANT: Jacobsen, Richard
/ APPLICANT: Jones, Robert M.
/ TITLE OF INVENTION: Omega-Conopeptides
/ FILE REFERENCE: 2314-241
/ CURRENT APPLICATION NUMBER: US/09/910,082A
/ CURRENT FILING DATE: 2001-07-23
/ PRIOR APPLICATION NUMBER: US 60/219,616
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: US 60/265,888
/ PRIOR FILING DATE: 2001-02-05
/ NUMBER OF SEQ ID NOS: 413
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 390
/ LENGTH: 27
/ TYPE: PRT
/ ORGANISM: Conus rattus
US-09-910-082A-390

Query Match      37.0%; Score 59.5; DB 10; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCN 22
   | : : : | | : : : | |
Db 1 CNARNDGCSQH-SQCCSGSCNK 21

RESULT 88
US-10-765-926-236
```

```
; Sequence 236, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; FILE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 236
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-236

Query Match      37.0%; Score 59.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLDDCCSRKCNR 22
Db      1 CNARNDGCSQH-SQCCSGSCNK 21

RESULT 90
US-09-910-082A-235
; Sequence 235, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 235
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-235

Query Match      37.0%; Score 59.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 5.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLDDCCSRKCNR 22
Db      48 CNARNDGCSQH-SQCCSGSCNK 68

RESULT 91
US-10-765-926-235
; Sequence 235, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 390
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-390

Query Match      37.0%; Score 59.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY      1 CRXNQKCFQHLDDCCSRKCNR 22
Db      1 CNARNDGCSQH-SQCCSGSCNK 21

RESULT 89
US-10-765-926-390
; Sequence 390, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 390
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-390
```

```
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent version 3.0
; SEQ ID NO 235
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-235

Query Match
Best Local Similarity 37.0%; Score 59.5; DB 16; Length 74;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKNCNR 22
Db 48 CNARNDCGCSQH-SQCCSGSCNK 68

RESULT 92
US-10-369-493-6999
; Sequence 6999, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6999
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6999

Query Match
Best Local Similarity 36.6%; Score 59; DB 15; Length 601;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKNCNRFNKCV 27
Db 120 CERNIDDCVNSKENGKCV 139

RESULT 93
US-10-289-776-9
; Sequence 9, Application US/10289776
; Publication No. US20030170727A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kid, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tessier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/10/289,776
; CURRENT FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: US/09/540,245
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/065,544
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 60/081,057
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 9
```

```
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-289-776-9
```

```
Query Match
Best Local Similarity 36.6%; Score 59; DB 14; Length 735;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKNCNRFNKCV 27
Db 254 CERNIDDCVNSKENGKCV 273
```

```
RESULT 94
US-09-910-082A-391
; Sequence 391, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: Patent version 3.0
; SEQ ID NO 391
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-391
```

```
Query Match
Best Local Similarity 36.3%; Score 58.5; DB 10; Length 27;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
```

```
QY 1 CRXNKCFOHLDCCSRKNCNR 22
Db 1 CNARNDCGCSQH-POCCSGSCNK 21
```

```
RESULT 95
US-09-910-082A-392
; Sequence 392, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
```



```
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 392
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-392

Query Match          36.3%; Score 58.5; DB 10; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNR 22
   | : | | | | | | | | | |
Db 1 CNARNSGCSQH-PQCCSGSCKN 21

RESULT 96
US-10-765-926-391
; Sequence 391, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 391
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-391

Query Match          36.3%; Score 58.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNR 22
   | : | | | | | | | | | |
Db 1 CNARNSGCSQH-PQCCSGSCKN 21

RESULT 97
US-10-765-926-392
; Sequence 392, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
```

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; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 392
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-392

Query Match          36.3%; Score 58.5; DB 16; Length 27;
Best Local Similarity 45.5%; Pred. No. 2.8;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNR 22
   | : | | | | | | | | | |
Db 1 CNARNSGCSQH-PQCCSGSCKN 21

RESULT 98
US-09-910-082A-238
; Sequence 238, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 238
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-238

Query Match          36.3%; Score 58.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNR 22
   | : | | | | | | | | | |
Db 48 CNARNSGCSQH-PQCCSGSCKN 68

RESULT 99
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US-09-910-082A-241
; Sequence 241, Application US/09910082A
; Publication No. US20030119731A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/09/910,082A
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 241
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-09-910-082A-241

Query Match 36.3%; Score 58.5; DB 10; Length 74;
Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
Qy 1 CRIXNOKCFOHLDCCSRKCNR 22
Db 48 CNARNSGCSQH-PQCCSGSCNK 68

RESULT 100
US-10-765-926-238
; Sequence 238, Application US/10765926
; Publication No. US20040132663A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Shon, Ki-Joon
; APPLICANT: Jacobsen, Richard
; APPLICANT: Jones, Robert M.
; APPLICANT: Cartier, G. Edward
; TITLE OF INVENTION: Omega-Conopeptides
; FILE REFERENCE: 2314-241
; CURRENT APPLICATION NUMBER: US/10/765,926
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 09/910,082
; PRIOR FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 60/219,616
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/265,888
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 238
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Conus rattus
US-10-765-926-238

Query Match 36.3%; Score 58.5; DB 16; Length 74;

Best Local Similarity 45.5%; Pred. No. 6.7;
Matches 10; Conservative 2; Mismatches 9; Indels 1; Gaps 1;
Qy 1 CRIXNOKCFOHLDCCSRKCNR 22
Db 48 CNARNSGCSQH-PQCCSGSCNK 68

Search completed: April 18, 2005, 20:43:01
Job time : 92.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:23:04 ; Search time 26.5 Seconds
(without alignments)

98.032 Million cell updates/sec

Title: US-10-627-685A-26

Perfect score: 161

Sequence: 1 CRXNQKCFQHLDDCCSKRKNRNV 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	27	2	kappa-conotoxin sv
2	71	44.1	26	2	omega-conotoxin pv
3	61	37.9	29	2	omega-conotoxin mv
4	59	36.6	601	2	hypothetical prote
5	59	36.6	601	2	protein F40E10.4 [
6	57	35.4	2524	2	Xotch protein - Af
7	56.5	35.1	194	2	lectin heavy chain
8	56.5	35.1	1292	2	galactose binding
9	56	34.8	2703	1	notch protein - fr
10	55.5	34.5	25	2	omega-conotoxin mv
11	55.5	34.5	194	2	lectin heavy chain
12	55	34.2	403	1	homeotic protein 1
13	55	34.2	404	2	LIM domain transcr
14	55	34.2	406	1	homeotic protein 1
15	55	34.2	406	1	homeotic protein 1
16	55	34.2	406	1	homeotic protein 1
17	55	34.2	406	1	homeotic protein 1
18	54.5	33.9	25	2	hypothetical prote
19	54.5	33.9	239	2	T24619
20	54.5	33.9	252	2	H97189
21	54	33.5	1372	2	T25933
22	53.5	33.2	572	2	T20764
23	53	32.9	277	2	B71406
24	53	32.9	2531	2	T31070
25	53	32.9	2555	2	A40043
26	52.5	32.6	474	2	T09688
27	52.5	32.6	1280	2	A39117
28	52	32.3	293	2	B26637
29	52	32.3	354	2	T22274

30	52	32.3	2139	2	A35672	crumbs protein - f
31	52	32.3	2471	2	A49128	cell-fate determin
32	52	32.3	2531	2	S18188	notch protein homo
33	52	32.3	2531	2	A46019	notch-1 protein -
34	51.5	32.0	29	2	A58537	omega-conotoxin mv
35	51.5	32.0	113	2	JC1088	propionyl acylase
36	51.5	32.0	1984	2	T13171	probable vitellog
37	51	31.7	29	2	A43620	omega-conotoxin gv
38	51	31.7	29	2	B43620	omega-conotoxin gv
39	51	31.7	53	2	T10405	conotoxin-like pro
40	51	31.7	53	2	T30499	conotoxin-like pro
41	51	31.7	100	2	S01348	acetylcholinester
42	51	31.7	358	2	E86452	protein F6N18.15 [
43	51	31.7	1687	2	T30176	EGF repeat transme
44	50.5	31.4	131	2	T25924	hypothetical prote
45	50.5	31.4	371	2	T23369	hypothetical prote
46	50.5	31.4	389	2	T46722	conserved hypotet
47	50.5	31.4	1208	2	T27822	hypothetical prote
48	50	31.1	53	2	C72850	conotoxin homolog
49	50	31.1	403	2	T28551	hypothetical prote
50	50	31.1	1474	2	T18281	hypothetical prote
51	50	31.1	1810	1	A32230	tenascin precursor
52	50	31.1	3623	2	T08618	intrinsic factor-B
53	49.5	30.7	37	2	A59457	I-superfamily cono
54	49.5	30.7	268	1	A30584	interleukin-1 beta
55	49.5	30.7	1282	2	JE0120	glycoprotein A - m
56	49.5	30.7	1516	2	T01055	hypothetical prote
57	49	30.4	194	2	T16556	hypothetical prote
58	49	30.4	395	2	T40102	conserved hypotet
59	49	30.4	427	2	G88492	protein T07E3.4 [i
60	49	30.4	833	2	T32289	hypothetical prote
61	49	30.4	846	2	A30889	integrin beta chal
62	49	30.4	1064	2	A40136	fibropellin Ia - s
63	49	30.4	1203	2	A49175	Notch B protein -
64	49	30.4	1291	2	T06692	hypothetical prote
65	49	30.4	1528	2	T08694	hypothetical prote
66	49	30.4	2318	2	S45306	notch 3 protein -
67	49	30.4	2437	2	S42612	transmembrane prot
68	48.5	30.1	124	1	NRCB	pancreatic ribonuc
69	48.5	30.1	128	2	J01739	hypothetical 14.7K
70	48.5	30.1	328	2	G89152	protein C24B5.5 [i
71	48.5	30.1	400	2	A45545	major merozoite su
72	48.5	30.1	461	2	T09341	hydroxymethylgluta
73	48.5	30.1	651	2	S47282	merozoite surface
74	48.5	30.1	1631	1	SAZQK1	major merozoite su
75	48.5	30.1	1639	2	S05603	major merozoite su
76	48.5	30.1	1701	2	A54498	major merozoite su
77	48.5	30.1	1726	1	SAZQGM	major merozoite su
78	48.5	30.1	1726	2	A45948	major merozoite su
79	48	29.8	49	2	S02007	protamine I - rabb
80	48	29.8	296	2	T26875	hypothetical prote
81	48	29.8	644	2	S64135	hypothetical prote
82	48	29.8	832	2	A31246	neurogenic protein
83	48	29.8	833	2	S15087	gene Delta protein
84	48	29.8	880	2	S00670	neurogenic repetit
85	48	29.8	1429	2	S06434	homeotic protein 1
86	48	29.8	2321	2	T78549	notch3 protein - h
87	48	29.8	3006	2	T28625	variant-specific s
88	48	29.8	4544	1	S02392	alpha-2-macroglobu
89	48	29.8	4545	1	S25111	alpha-2-macroglobu
90	47.5	29.5	124	1	NRDEN	pancreatic ribonuc
91	47.5	29.5	196	2	A39384	finger protein HPP
92	47.5	29.5	249	2	H72858	apoptosis inhibito
93	47.5	29.5	249	2	T41814	IAP2 orf71 - Bomby
94	47.5	29.5	253	2	A49371	repB protein - Cam
95	47.5	29.5	595	2	G02075	transcription repr
96	47	29.2	285	2	T20506	hypothetical prote
97	47	29.2	295	2	AG3129	transcription regu
98	47	29.2	295	2	B98158	agpt protein (AF23
99	47	29.2	351	2	B71604	rRNA methylase (Sp
100	47	29.2	365	2	T26564	hypothetical prote

RESULT 3

RESULT 3

omega-conotoxin MVIIIC precursor [validated] - cone shell (Conus magus) (fragment)
C:Species: Conus magus (magus cone)
C:Date: 17-Apr-1993 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004
C:Accession: JH0699; PC2380
R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadaasdi, L.; Ramachandran, J.; N
Neuron 9, 69-77, 1992
A:Title: A new conus peptide ligand for mammalian presynaptic Ca2+ channels.
A:Reference number: JH0699; MUID:92337922; PMID:1352986
A:Accession: JH0699
A:Molecule type: mRNA
A:Residues: 1-29 <HL>
A:Cross-references: UNIPROT:P37300; GB:S40826; NID:G952126; PION:AAB22674.1; PID:G952126
R:Nemoto, N.; Kubo, S.; Yoshida, T.; Chino, N.; Kimura, T.; Sakakibara, S.; Kyogoku, Y.
Biochem. Biophys. Res. Commun. 207, 695-700, 1995
A:Title: Solution structure of omega-conotoxin MVIIIC determined by NMR.
A:Reference number: PC2380; MUID:95169113; PMID:7664862
A:Accession: PC2380
A:Molecule type: protein
A:Residues: 3-28 <NM>
R:Farri-Jones, S.; Basus, V.J.
submitted to the Brookhaven Protein Data Bank, December 1994
A:Reference number: A66297; PDB:1OMN
A:Contents: annotation; conformation by (1)H-NMR, residues 3-28
R:Farri-Jones, S.; Miljanich, G.P.; Nadaasdi, L.; Ramachandran, J.; Basus, V.J.
J. Mol. Biol. 248, 106-124, 1995
A:Title: Solution structure of omega-conotoxin MVIIIC, a high affinity of P-type calcium
A:Reference number: A38582; MUID:95248539; PMID:7731037
A:Contents: annotation; conformation by (1)H-NMR

C; Keyword

C;Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh
F:3-28/Product: omega-conotoxin MVIC #status experimental <MAT>
F:3-16,10-22,17-28/Dissulfide bonds: #status experimental
F:28/Modified site: amidated carboxyl end (Cys) (amide in mature form from following gly

Query Match 37.9%; Score 61; DB 2; Length 29;
Best Local Similarity 38.5%; Pred.No.1.1;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Oy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 26
| : | : | : | : | : | :
db 3 CKRGAPCRKTMYDCCSGSCGRRGKC 28

RESIST. 4

```

RESULT 4
T22025
Hypothetical protein F40E10.4 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22025
R:Smyle, R.
Submitted to the EMBL Data Library, February 1996
A:Reference number: Z19503
A:Accession: T22025
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-601 <WIL>
A:Cross-references: UNIPROT:Q20204; EMBL:Z69792; PIDN:CAA93668.1; GSPDB:GN00028; CESP:F40E10.4
A:Experimental source: Clone F40E10
A:Genetics:
A:Gene: CESP:F40E10.4
A:Map position: X

Query Match      36.6%; Score 59; DB 2; Length 601;
Best Local Similarity 45.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

          8 CFOHLLDCCSRKCRNFKNKV 27
          |::|||::|||
120 CERNIDDCVNSKENGKGV 139

```

```
RESULT 5
D89711
Protein F40E10.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89711
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: D89711
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-601 <STO>
A;Cross-references: UNIPROT:Q20204; GB:chr_X; PIDN:CAA93668.1; PID:g3877014; GSPDB:GN000
C;Genetics:
A;Gene: F40E10.4
A;Map position: X

Query Match 36.6%; Score 59; DB 2; Length 601;
Best Local Similarity 45.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRRNKCV 27
Db 120 CEKNIDDCVNSKCGNGKCV 139
|::|||::|||
|::|||::|||

RESULT 6
A35844
Xotch protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 16-Aug-2004
C;Accession: A35844
R;Coffman, C.; Harris, W.; Kintner, C.
Science 249, 1438-1441, 1990
A;Title: Xotch, the Xenopus homolog of Drosophila notch.
A;Reference number: A35844; MUID:90385285; PMID:2402639
A;Accession: A35844
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-2524 <COF>
C;Superfamily: Notch protein; ankyrin repeat homology; EGF homology
C;Keywords: transmembrane protein
F;146-177/Domain: EGF homology <EGX1>
F;184-215/Domain: EGF homology <EGF1>
F;222-254/Domain: EGF homology <EGF>
F;456-487/Domain: EGF homology <EGX2>
F;757-788/Domain: EGF homology <EGF3>
F;1025-1056/Domain: EGF homology <EGX3>
F;1924-1956/Domain: ankyrin repeat homology <AN1>
F;1957-1989/Domain: ankyrin repeat homology <AN2>
F;1991-2023/Domain: ankyrin repeat homology <AN3>
F;2024-2056/Domain: ankyrin repeat homology <AN4>
F;2057-2089/Domain: ankyrin repeat homology <AN5>

Query Match 35.4%; Score 57; DB 2; Length 2524;
Best Local Similarity 37.5%; Pred. No. 58;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNQCQFQHLDDCCSRKCNRRNKCV 27
Db 250 SGQNCENIDDCFSNNCRNGTCV 273
|::|||::|||
|::|||::|||

RESULT 7
S70663
lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)
C;Species: Entamoeba histolytica
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70663
```

```
R;Ramakrishnan, G.; Regland, B.D.; Purdy, J.E.; Mann, B.J.
Mol. Microbiol. 19, 91-100, 1996
A;Title: Physical mapping and expression of gene families encoding the N-acetyl D-galact
A;Reference number: S70662; MUID:96419166; PMID:8821939
A;Accession: S70663
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-194 <RAM>
A;Cross-references: UNIPROT:Q24821; EMBL:U33443; NID:g993052; PID:g993053
C;Genetics:
A;Gene: bg14

Query Match 35.1%; Score 56.5; DB 2; Length 194;
Best Local Similarity 43.3%; Pred. No. 12;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 119 CSMGTDTNIIYHDDCNRSKSCQCNFNGKCV 148
|::|||::|||
|::|||::|||

RESULT 8
T09229
galactose binding adhesin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09229
R;Purdy, J.E.; Mann, B.J.; Shugart, E.C.; Petri, W.A.
Mol. Biochem. Parasitol. 62, 53-59, 1993
A;Title: Analysis of the gene family encoding the Entamoeba histolytica galactose-specifi
A;Reference number: Z16622; MUID:94158976; PMID:8114826
A;Accession: T09229
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-1292 <PUR>
A;Cross-references: UNIPROT:Q24835; EMBL:L14815; NID:g290648; PID:g290649
C;Genetics:
A;Gene: bg13
C;Keywords: lectin

Query Match 35.1%; Score 56.5; DB 2; Length 1292;
Best Local Similarity 43.3%; Pred. No. 43;
Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
Db 718 CSMGTDTNIIYHDDCNRSKSCQCNFNGKCV 747
|::|||::|||
|::|||::|||

RESULT 9
A24420
notch protein - fruit fly (Drosophila melanogaster)
N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Aug-2004
C;Accession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624; PMID:3097517
A;Accession: A24420
A;Molecule type: DNA
A;Residues: 1-2703 <KID>
A;Cross-references: UNIPROT:P07207; GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A;Reference number: A24768; MUID:86079539; PMID:3935325
A;Accession: A24768
A;Molecule type: mRNA
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958,'
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R;Tautz, D.
Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
```

A:Reference number: S09358; MUID:89385974; PMID:2780284

A:Accession: S09358

A:Molecule type: DNA

A:Residues: 2505-2551, 'QQQ', 2552-2576, 'E', 2578-2604 <TAU>

R:Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Taoukas, S.

Cell 40, 55-62, 1985

A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other

A:Reference number: A05267; MUID:85099329; PMID:2981631

A:Accession: A05267

A:Molecule type: DNA

A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>

C:Genetics:

A:Gene: notch; opa

A:Cross-references: FlyBase:FBgn0004647

A:Map position: 8, 96-9, 36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3

C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C:Keywords: differentiation; tandem repeat; transmembrane protein

F:27-43/Domain: transmembrane #status predicted <TMM1>

F:297-328/Domain: EGF homology <EGX1>

F:530-561/Domain: EGF homology <EGF1>

F:568-599/Domain: EGF homology <EGF>

F:988-1019/Domain: EGF homology <EGX2>

F:1064-1095/Domain: EGF homology <EGF3>

F:1187-1218/Domain: EGF homology <EGX3>

F:1746-1762/Domain: transmembrane #status predicted <TMM2>

F:1950-1982/Domain: ankyrin repeat homology <AN1>

F:1983-2015/Domain: ankyrin repeat homology <AN2>

F:1988-2004/Domain: transmembrane #status predicted <TMM3>

F:2017-2049/Domain: ankyrin repeat homology <AN3>

F:2050-2082/Domain: ankyrin repeat homology <AN4>

F:2083-2115/Domain: ankyrin repeat homology <AN5>

F:2538-2568/Region: glutamine-rich

F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 34.8%; Score 56; DB 1; Length 2703;

Best Local Similarity 33.3%; Pred. No. 79;

Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFKNCV 27

DB 822 TGGKCTNIDCVNPGNGGTCTC 845

RESULT 10

JH0701

omega-conotoxin MVIIB - cone shell (Conus magus)

C:Species: Conus magus (magus cone)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C:Accession: JH0701; B34115

R:Hillyard, D.R.; Monje, V.D.; Mintz, I.M.; Bean, B.P.; Nadasdi, L.; Ramachandran, J.; M

Neuron 9, 69-77, 1992

A:Title: A new conus peptide ligand for mammalian presynaptic Ca²⁺ channels.

A:Reference number: JH0699; MUID:92337922; PMID:1352986

A:Accession: JH0701

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-25 <HIL>

A:Cross-references: UNIPROT:P05485

R:Olivera, B.M.; Cruz, L.J.; de Santos, V.; LeCheminant, G.W.; Griffin, D.; Zeikus, R.;

Biochemistry 26, 2086-2090, 1987

A:Title: Neuronal calcium channel antagonists. Discrimination between calcium channel su

A:Reference number: B34115; MUID:87299637; PMID:2441741

A:Accession: B34115

A:Molecule type: protein

A:Residues: 1-25 <OLI>

C:Superfamily: omega-conotoxin

C:Keywords: acetylcholine release inhibition; amidated carboxyl end; calcium channel inh

F:1-16, 8-20, 15-45/disulfide bonds: #status predicted

F:25/Modified site: amidated carboxyl end (Cys) #status predicted

Query Match

Best Local Similarity 34.5%; Score 55.5; DB 2; Length 25;

Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKCNRFKNC 26

DB 1 CKKGASCHRTSYDCCGTGSCNR-GKC 25

RESULT 11

S70664

lectin heavy chain, N-acetylgalactosamine-specific - Entamoeba histolytica (fragment)

C:Species: Entamoeba histolytica

C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S70664

R:Ramakrishnan, G.; Ragland, B.D.; Purdy, J.E.; Mann, B.J.

Mol. Microbiol. 19, 91-100, 1996

A:Title: Physical mapping and expression of gene families encoding the N-acetyl D-galact

A:Reference number: S70662; MUID:96419166; PMID:8821939

A:Accession: S70664

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-194 <RAM>

A:Cross-references: UNIPROT:Q24822; EMBL:U33444; NID:g993054; PID:g993055

C:Genetics:

A:Gene: hgl5

Query Match

Best Local Similarity 34.5%; Score 55.5; DB 2; Length 194;

Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRK--CNRFN-KCV 27

DB 119 CSMTGDNVITYHDDCNRSKQCGNFGKCI 148

RESULT 12

S23802

homeotic protein lim-1 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S23802

R:Taira, M.; Jamrich, M.; Good, P.J.; Dawid, I.B.

Genes Dev. 6, 356-366, 1992

A:Title: The LIM domain-containing homeo box gene Xlim-1 is expressed specifically in the

A:Reference number: S23802; MUID:92192449; PMID:1347750

A:Accession: S23802

A:Molecule type: mRNA

A:Residues: 1-403 <TAI>

A:Cross-references: UNIPROT:P29674; EMBL:X63889; NID:g64829; PIDN:CAA45353.1; PID:g64830

C:Genetics:

A:Gene: lim-1

C:Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homol

C:Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulatio

F:4-54/Domain: LIM metal-binding repeat homology <LIM1>

F:63-117/Domain: LIM metal-binding repeat homology <LIM2>

F:180-236/Domain: homeobox homology <HOX>

Query Match

Best Local Similarity 34.2%; Score 55; DB 1; Length 403;

Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRFKNC 26

DB 22 RAWHKVCVQ---CCECKNLTEKC 42

RESULT 13

G01507

LIM domain transcription factor LIM-1 - human

N:Alternate names: homeotic protein lim-1

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004

C:Accession: G01507

R:Dong, W.

submitted to the EMBL Data Library, September 1994

A;Reference number: G07570
A;Accession: G01507
C;Superfamily: homeotic protein lim-1 - golden hamster
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-404 <DON>
A;Cross-references: UNIPROT:P48742; EMBL:U14755; NID:G549845; PIDN:AAA21644.1; PID:G549845
C;Genetics:

A;Gene: hlim-1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 2; Length 404;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNKCFOHLDCCSRKCNRFNK 26
| : : | | | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTKEC 42

RESULT 14

I58187
homeotic protein lim-1 - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I58187

R;Furuyama, T.; Inagaki, S.; Iwahashi, Y.; Takagi, H.
Neurosci. Lett. 170, 266-268, 1994
A;Title: Distribution of Rlim, an LIM homeodomain gene, in the rat brain.
A;Reference number: I58187; MUID:94336075; PMID:7914684
A;Accession: I58187
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: GB:S71523; NID:G559635; PIDN:AAC60696.1; PID:G559636
C;Genetics:

A;Gene: lim-1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNKCFOHLDCCSRKCNRFNK 26
| : : | | | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTKEC 42

RESULT 15

I48186
homeotic protein lim-1 - golden hamster
N;Alternate names: homeotic protein lim2
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48186

R;Rudnick, A.; Ling, T.Y.; Odagiri, H.; Rutter, W.J.; German, M.S.
Proc. Natl. Acad. Sci. U.S.A. 91, 12203-12207, 1994
A;Title: Panceratic beta cells express a diverse set of homeobox genes.
A;Reference number: I48186; MUID:95083670; PMID:7991607
A;Accession: I48186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: UNIPROT:P36199; EMBL:X81407; NID:G587462; PIDN:CAA57164.1; PID:G587462
C;Genetics:

A;Gene: lmx2

C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNKCFOHLDCCSRKCNRFNK 26
| : : | | | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTKEC 42

RESULT 16

I48637
homeotic protein lim-1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48637; S42788

R;Fujii, T.; Pichel, J.G.; Taira, M.; Toyama, R.; David, I.B.; Westphal, H.
Dev. Dyn. 199, 73-83, 1994
A;Title: Expression patterns of the murine LIM class homeobox gene lim1 in the developing embryo.
A;Reference number: I48637; MUID:94220754; PMID:7909459
A;Accession: I48637

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <RES>
A;Cross-references: UNIPROT:P36199; EMBL:Z27410; NID:G425216; PIDN:CAA81797.1; PID:G425217

R;Fujii, T.
submitted to the EMBL Data Library, November 1993
A;Reference number: S42788

A;Accession: S42788
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-406 <FUF>
A;Cross-references: EMBL:Z27410; NID:G425216; PIDN:CAA81797.1; PID:G425217
C;Genetics:

A;Gene: lhx1
C;Superfamily: homeotic protein lim-1; homeobox homology; LIM metal-binding repeat homology
C;Keywords: DNA binding; duplication; embryo; homeobox; nucleus; transcription regulation
F;4-54/Domain: LIM metal-binding repeat homology <LIM1>
F;63-117/Domain: LIM metal-binding repeat homology <LIM2>
F;181-237/Domain: homeobox homology <HOX>

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 29;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNKCFOHLDCCSRKCNRFNK 26
| : : | | | | | | | | | |
Db 22 RAWHVKCVQ-----CCECKCNLTKEC 42

RESULT 17

I50375
homeotic protein lim-1 - chicken

C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50375
R;Tsuchida, T.; Ensign, M.; Morton, S.B.; Baldassare, M.; Edlund, T.; Jessell, T.M.; Pfa.
Cell 79, 957-970, 1994

A;Title: Topographic organization of embryonic motor neurons defined by expression of LIM
A;Reference number: A55198; MUID:95094281; PMID:7528105
A;Accession: I50375

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-406 <TSU>
A;Cross-references: UNIPROT:P53411; GB:I35569; NID:G531182; PIDN:AAA62173.1; PID:G531183
C;Genetics:

A;Gene: lim-1

1 CRINQKCFQLDDCCSRKCNFNKC 26
::: |||:
1 CKGGAKCRLMYDCCTGSC-RSGKC 25

A;Residues: 1-1372 <MUR>
A;Cross-references: UNIPROT:P91526; EMBL:U80815; PIDN:AAB37995.1; GSPDB:GN00022; CESP:W02C12
A;Experimental source: strain Bristol N2; clone W02C12
C;Genetics:
A;Gene: CESP:W02C12.1
A;Map position: 4
A;Introns: 29/1; 66/1; 774/2; 823/2; 1046/1; 1108/2; 1298/1

Query Match 33.5%; Score 54; DB 2; Length 1372;
Best Local Similarity 29.2%; Pred.No. 85;
Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNKCV 27
 : : | : | : | : | :
Db 95 TGENCDQNIDECASPCQNDACKI 118

RESULT 22
T20764
hypothetical protein Fllc1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20764
R;Palmer, S.
submitted to the EMBL Data Library, September 1995
A;Reference number: Z19321
A;Accession: T20764
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-572 <WIL>
A;Cross-references: UNIPROT:Q19345; EMBL:Z54270; PIDN:CAA91028.1; GSPDB:GN00028; CESP:FI1C1
A;Experimental source: clone Fllc1
C;Genetics:
A;Gene: CESP:Fllc1.6
A;Map position: X
A;Introns: 39/3; 50/3; 87/1; 148/2; 190/1; 286/1; 377/3; 417/2; 499/2
C;Superfamily: steroid hormone receptor Ad4BP; erba transforming protein homology

Query Match 33.2%; Score 53.5; DB 2; Length 572;
Best Local Similarity 32.4%; Pred.No. 54;
Matches 11; Conservative 8; Mismatches 6; Indels 9; Gaps 2;

QY 3 IXNOKCFQ-----HLDCCSRKCNC--RFNKCV 27
 : : | : | : | : | :
Db 46 VQNKQYQCSEAANCHVDTRCKRCPCRFQKCL 79

RESULT 23
B71406
hypothetical protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C;Accession: B71406
R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel, A.; Schaeffer, M.; Funk, B.
nature 391, 485-488, 1998
A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, J.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Anthonioff, A.; Moore, T.
C;Chalwatiz, N.
A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: B71406
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-277 <BEV>
A;Cross-references: UNIPROT:O23297; GB:Z97336; NID:g2244788; PID:e327451; PID:g2244797
C;Genetics:
A;Map position: 4COP9-4G3845

Query Match 32.9%; Score 53; DB 2; Length 277;
Best Local Similarity 59.8%; Pred.No. 38;

N:Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase
 C:Species: Pinus sylvestris (Scotch pine)
 C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: T09688
 R:Wegener, A.; Gimbel, W.; Werner, T.; Hani, J.; Ernst, D.; Sandermann, H.
 Biochim. Biophys. Acta 1350, 247-252, 1997
 A>Title: Molecular cloning of ozone-inducible protein from Pinus sylvestris L. with high
 A:Reference number: Z16823, MUID:97214637, PMID:9061017
 A:Accession: T09688
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-474 <WEG>
 A:Cross-references: UNIPROT:P93773; EMBL:X96386; NID:G1655678; PIDN:CAA65250.1; PID:G1655678
 A:Experimental source: tissue-type needles
 C:Function:
 A:Description: catalyzes the condensation of acetyl coenzyme A (Ac-CoA) with acetoacetylase
 C:Superfamily: hydroxymethylglutaryl-CoA synthase
 C:Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase

Query Match 32.6%; Score 52.5; DB 2; Length 474;
 Best Local Similarity 43.5%; Pred. No. 62;
 Matches 10; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

QY 4 XNOKCF-QHLDCCSRKCNRFNK 25
 DB 211 LSQTCYLMALDSYKRCNKFKEK 233

RESULT 27
 A39117
 170K lectin precursor - Entamoeba histolytica (fragment)
 C:Species: Entamoeba histolytica
 C>Date: 30-Aug-1991 #sequence_revision 17-Apr-1993 #text_change 09-Sep-1997
 C:Accession: A39117
 R:Tannich, E.; Ebert, F.; Horstmann, R.D.
 Proc. Natl. Acad. Sci. U.S.A. 88, 1849-1853, 1991
 A>Title: Primary structure of the 170-kDa surface lectin of pathogenic Entamoeba histolytica
 A:Reference number: A39117; MUID:91156704; PMID:2000392
 A:Accession: A39117
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1280 <TAN>
 A:Cross-references: GB:M60498; NID:G158958; PID:G158959
 C:Keywords: transmembrane protein

Query Match 32.6%; Score 52.5; DB 2; Length 1280;
 Best Local Similarity 41.4%; Pred. No. 1.2e+02;
 Matches 12; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKCQFQHLDDCCSRK--CNRFN-KC 26
 DB 705 CSMGTDNVITYHDDCCSRKSCQGNFNGKC 733

RESULT 28
 B26637
 neurogenic repetitive locus 95F protein - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
 C:Accession: B26637
 R:Knuet, E.; Dietrich, U.; Tepass, U.; Brenner, K.A.; Weigel, D.; Vaessin, H.; Campos-Ord
 EMO J. 6, 761-766, 1987
 A>Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
 A:Reference number: A91081; MUID:87218537; PMID:3107986
 A:Accession: B26637
 A:Molecule type: mRNA
 A:Residues: 1-293 <KNU>
 A:Cross-references: UNIPROT:P10040; GB:X05144; NID:G7519; PIDN:CAA28793.1; PID:G929536
 A:Gene: FlyBase:crb
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0000368
 C:Keywords: transmembrane protein

F:139-170/Domain: EGF homology <EGX1>
 F:177-208/Domain: EGF homology <EGF1>
 F:216-252/Domain: EGF homology <EGF>

Query Match 32.3%; Score 52; DB 2; Length 293;
 Best Local Similarity 30.4%; Pred. No. 52;
 Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNK 26
 DB 166 EGQHCQNIDECADQPCNNGNC 188

RESULT 29
 T22274
 hypothetical protein F46B3.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22274
 R:Ainscough, R.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19541
 A:Accession: T22274
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-354 <WIL>
 A:Cross-references: UNIPROT:Q9XV21; EMBL:Z81540; PIDN:CAB04398.1; GSPDB:GN00023; CESP:F46B3
 A:Experimental source: clone F46B3
 C:Genetics:
 A:Gene: CESP:F46B3.9
 A:Map position: 5
 A:Introns: 23/1; 55/1; 82/1; 112/1; 142/1; 170/1; 193/1; 223/1; 299/1

Query Match 32.3%; Score 52; DB 2; Length 354;
 Best Local Similarity 35.7%; Pred. No. 58;
 Matches 10; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

QY 1 CRIXN--OKCFQHLDDCCSRKCNRFNK 26
 DB 158 CLKVNGSPKCVPELDQCCKSHIKCSIGSHC 185

RESULT 30
 A35672
 crumbs protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 21-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004
 C:Accession: A35672
 R:Tepass, U.; Theres, C.; Knuet, E.
 Cell 61, 787-799, 1990
 A>Title: crumbs encodes an EGF-like protein expressed on apical membranes of Drosophila
 A:Reference number: A35672; MUID:90263104; PMID:2344615
 A:Accession: A35672
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-2139 <TEP>
 A:Cross-references: UNIPROT:P10040; GB:M33753
 A:Note: the authors translated the codon GGC for residue 1928 as Cys, and TAT for residue
 C:Genetics:
 A:Gene: FlyBase:crb
 A:Cross-references: FlyBase:FBgn0000368
 C:Keywords: transmembrane protein
 F:352-385/Domain: EGF homology <EGX1>
 F:392-424/Domain: EGF homology <EGF1>
 F:691-722/Domain: EGF homology <EGF>
 F:767-799/Domain: EGF homology <EGF3>
 F:1878-1914/Domain: EGF homology <EGX2>

Query Match 32.3%; Score 52; DB 2; Length 2139;
 Best Local Similarity 30.4%; Pred. No. 1.9e+02;
 Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKCNRFNK 26

Query Match	32.0%	Score 51.5;	DB 2;	Length 113;
Best Local Similarity	33.3%	Pred. No. 31;		

1	:	1
2	:	1
3	:	1
4	:	1
5	:	1
6	:	1
7	:	1
8	:	1
9	:	1
10	:	1
11	:	1
12	:	1
13	:	1
14	:	1
15	:	1
16	:	1
17	:	1
18	:	1
19	:	1
20	:	1
21	:	1
22	:	1
23	:	1
24	:	1
25	:	1
26	:	1
27	:	1
28	:	1
29	:	1
30	:	1
31	:	1
32	:	1
33	:	1
34	:	1
35	:	1
36	:	1
37	:	1
38	:	1
39	:	1
40	:	1
41	:	1
42	:	1
43	:	1
44	:	1
45	:	1
46	:	1
47	:	1
48	:	1
49	:	1
50	:	1
51	:	1
52	:	1
53	:	1
54	:	1
55	:	1
56	:	1
57	:	1
58	:	1
59	:	1
60	:	1
61	:	1
62	:	1
63	:	1
64	:	1
65	:	1
66	:	1
67	:	1
68	:	1
69	:	1
70	:	1
71	:	1
72	:	1
73	:	1
74	:	1
75	:	1
76	:	1
77	:	1
78	:	1
79	:	1
80	:	1
81	:	1
82	:	1
83	:	1
84	:	1
85	:	1
86	:	1
87	:	1
88	:	1
89	:	1
90	:	1
91	:	1
92	:	1
93	:	1
94	:	1
95	:	1
96	:	1
97	:	1
98	:	1
99	:	1
100	:	1

A schematic diagram of a 1D lattice chain. The chain is represented by a horizontal line with several vertical tick marks indicating sites. One site is highlighted with a dot and a vertical line. A small 'a' is placed below the chain, representing the lattice constant.

EGF repeat transmembrane protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30176
R:Sell, C.; Hoff III, H.B.
submitted to the EMBL Data Library, May 1996
A:Description: Cloning of a novel mRNA regulated by the insulin like growth factor type
A:Reference number: Z20762
A:Accession: T30176
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1687 <SEL>
A:Cross-references: UNIPROT:Q61204; EMBL:U57368; NID:G1336627; PID:G1336628; PIDN:AAB013
A:Experimental source: strain C57BL/6J; clone DBI-1; whole embryo

Query Match 31.7%; Score 51; DB 2; Length 1687;
Best Local Similarity 40.0%; Pred. No. 2.1e+02;
Matches 8; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFQHLDDCCSRKCNRFKNCV 27
DB 486 CERNIDCPNHKQCGGVCV 505
:::|||||::|

RESULT 44
T25924
hypothetical protein T27E4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25924
R:Bradehaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid T27E4.
A:Reference number: Z20111
A:Accession: T25924
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-131 <BRA>
A:Cross-references: UNIPROT:Q23053; EMBL:U64837; PIDN:AAB04836.1; GSPDB:GN00023; CESP:T2
A:Experimental source: strain Bristol N2; clone T27E4
C:Genetics:
A:Gene: CESP:T27E4.5
A:Map position: 5
A:Introns: 40/1; 53/2; 98/1; 118/3

Query Match 31.4%; Score 50.5; DB 2; Length 131;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 9; Conservative 4; Mismatches 13; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFKNCV 27
DB 80 CKTDQCMFSNVQKCCDAGCG-FNVCV 105
:::|||||::|

RESULT 45
T23369
hypothetical protein K06B4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23369
R:Lloyd, C.
submitted to the EMBL Data Library, December 1996
A:Reference number: Z19732
A:Accession: T23369
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-371 <WIL>
A:Cross-references: UNIPROT:Q17932; EMBL:Z83233; PIDN:CAB05765.1; GSPDB:GN00023; CESP:K0
A:Experimental source: clone K06B4
C:Genetics:
A:Gene: CESP:K06B4.5
A:Map position: 5
A:Introns: 8/3; 120/3; 242/1

Query Match 31.4%; Score 50.5; DB 2; Length 371;
Best Local Similarity 42.3%; Pred. No. 89;
Matches 11; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFKNCV 26
DB 31 CRNINO-CFQVNSPIKCRACRFKNCV 55
:::|||||::|

RESULT 46
T46722
conserved hypothetical protein [imported] - Leishmania major
N:Alternate names: probable proline synthetase associated protein
C:Species: Leishmania major
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C:Accession: T46722
R:Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1999
A:Reference number: Z23137
A:Accession: T46722
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-389 <VOL>
A:Cross-references: UNIPROT:Q9U147; EMBL:AL121861; PIDN:CAB58387.1
A:Experimental source: strain Friedlin
C:Genetics:
A:Note: L4326.11

Query Match 31.4%; Score 50.5; DB 2; Length 389;
Best Local Similarity 60.0%; Pred. No. 92;
Matches 9; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 8 CFQHLDDCCSRKCNRFKNCV 22
DB 84 CLCHV-DCCSRRCFR 97
:::|||||::|

RESULT 47
T27822
hypothetical protein ZK287.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27822
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z20425
A:Accession: T27822
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1208 <WIL>
A:Cross-references: UNIPROT:Q23456; EMBL:Z70757; PIDN:CAA94800.1; GSPDB:GN00023; CESP:ZK
A:Experimental source: clone ZK287
C:Genetics:
A:Gene: CESP:ZK287.4
A:Map position: 5
A:Introns: 44/1; 131/3; 167/1; 259/1; 319/1; 355/1; 484/3; 713/3; 765/1; 840/2; 1036/1; 1

Query Match 31.4%; Score 50.5; DB 2; Length 1208;
Best Local Similarity 47.8%; Pred. No. 1.9e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 1; Gaps 1;

QY 4 XNQCFOHLDCCSRKCNRFKNCV 26
DB 804 GNQNFQSFDS-CSRACGATNVC 825
:::|||||::|

RESULT 48
C72850
conotoxin homolog - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A:Note: dsDNA virus
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

A;Residues: 1-1474 <R>
A;Cross-references: UNIPROT:Q23870; EMBL:U00796; NID:g2702254; PID:g2702256; PIDN:AAC186
C;Genetics:
A;Introns: 33/2

Query Match 31.1%; Score 50; DB 2; Length 1474;
Best Local Similarity 52.9%; Pred. No. 2.5e+02;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKC 20
 :::-|||:::-|||
Db 1449 LNQECKULHLCQCSKKC 1465

RESULT 51
A32230
tenascin precursor - chicken
N;Alternate names: cytotoxin; hexabrachion
N;Contains: tenascin 190K; tenascin 200K
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
C;Accession: A32230; B32230; A33379; C33379; S01292; A30903
R;Jones, F.S.; Hoffman, S.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A;Title: A detailed structural model of cytotoxin: protein homologies, alternative RNA
A;Reference number: A32230; MUID:89184536; PMID:2467292
A;Accession: A32230
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1810 <JON>
A;Cross-references: UNIPROT:Q90824; GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
A;Accession: B32230
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1044,1318-1810 <JO2>
A;Cross-references: GB:J04519
R;Spring, J.; Beck, K.; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A;Title: Two contrary functions of tenascin: dissection of the active sites by recombinar
A;Reference number: A33379; MUID:90030407; PMID:2478295
A;Accession: A33379
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-204,'G','206-221','A','223-380','D','382-386','H','388-444','HN','447-450','V','452-5'
A;Cross-references: GB:M23121; NID:g212746; PIDN:AAA49086.1; PID:g212749
A;Accession: B33379
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-204,'G','206-221','A','223-380','D','382-386','H','388-444','HN','447-450','V','452-5'
A;Accession: C33379
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-204,'G','206-221','A','223-380','D','382-386','H','388-444','HN','447-450','V','452-5'
A;Cross-references: GB:M23121
R;Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R.
EMBO J. 7, 2977-2982, 1988
A;Title: Tenascin: cDNA cloning and induction by TGF-beta.
A;Reference number: S01292; MUID:89030589; PMID:2460335
A;Accession: S01292
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 27-181,'R','183-204','G','206-221','A','223-380','D','382-386','H','388-444','HN','447-4'
A;Cross-references: EMBL:X08030
A;Note: part of this sequence was confirmed by protein sequencing
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type I
C;Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-33/Domain: propeptide #status predicted <PRO>
F;34-1810/Product: tenascin 230K #status predicted <MAT>
F;223-249/Domain: EGF homology <EGF1>
F;316-342/Domain: EGF homology <EGF>
F;592-673/Domain: fibronectin type III repeat homology <FN3A>
F;681-765/Domain: fibronectin type III repeat homology <FN3B>

F;773-857/Domain: fibronectin type III repeat homology <FN3C>
 F;865-949/Domain: fibronectin type III repeat homology <FN3D>
 F;957-1037/Domain: fibronectin type III repeat homology <FN3E>
 F;1046-1128/Domain: fibronectin type III repeat homology <FN3F>
 F;1137-1219/Domain: fibronectin type III repeat homology <FN3G>
 F;1228-1310/Domain: fibronectin type III repeat homology <FN3H>
 F;1318-1399/Domain: fibronectin type III repeat homology <FN3I>
 F;1407-1487/Domain: fibronectin type III repeat homology <FN3J>
 F;1495-1575/Domain: fibronectin type III repeat homology <FN3K>
 F;1590-1798/Domain: fibronectin type III repeat homology <FN3L>
 F;1734-1747/Domain: calcium binding/gamma homology <FGB>
 F;1734-1747/Domain: calcium binding/gamma homology <FGB>

Query Match 31.1%; Score 50; DB 1; Length 1810;
 Best Local Similarity 35.3%; Pred. No. 2.9e+02;
 Matches 12; Conservative 3; Mismatches 11; Indels 8; Gaps 2;

QY 2 RIXNOKCFQHL-----DDC-----CSRKNRFRNKC 27
 Db 356 RCENGLCVCHGFGVDDCSQRCPKTCNNGRCV 389

RESULT 52

T08618
 Intrinsic factor-B12 receptor CUBILIN precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T08618
 F;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Biol. Chem. 273, 5235-5242, 1998
 A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
 A;Reference number: 216459; MUID:98148073; PMID:9478979
 A;Accession: T08618
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-3623 <MOE>
 A;Cross-references: UNIPROT:O70244; EMBL:AF022247; NID:G3834379; PIDN:AACT1661.1; PID:G3834379
 C;Genetics:
 A;Gene: CUBILIN
 C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
 C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-3623/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
 F;133-164/Domain: EGF homology <EGF1>
 F;436-467/Domain: EGF homology <EGF>

Query Match 31.1%; Score 50; DB 2; Length 3623;
 Best Local Similarity 29.2%; Pred. No. 4.6e+02;
 Matches 7; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNOKCFQHLDDCCSRKNRFRNKC 27
 Db 425 SGQNCENINDCSSNPLNGGTCI 448

RESULT 53

A59457
 I-superfamily conotoxin rille - Conus radiatus
 C;Species: Conus radiatus
 C;Date: 20-Jan-2003 #sequence_revision 20-Jan-2003 #text_change 09-Jul-2004
 C;Accession: A59457
 R;Olivera, B.
 submitted to the Protein Sequence Database, January 2003
 A;Description: Novel Excitatory Conus Peptides Define a New Conotoxin Superfamily.
 A;Reference number: A59457
 A;Accession: A59457
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-37 <OLI>
 A;Cross-references: UNIPROT:Q7M4K5
 A;Note: Injection of rille in 13- to 15-day-old mice caused hyperactivity, circular motile
 ward swimming or swimming in a vertical direction and death.
 F;13/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted
 F;14/Modified site: gamma-carboxyglutamic acid (Glu) #status predicted

F;34/Modified site: 6-bromotryptophan (Trp) #status predicted
 Query Match 30.7%; Score 49.5; DB 2; Length 37;
 Best Local Similarity 30.8%; Pred. No. 25;
 Matches 8; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKNRFRNKC 26
 Db 2 CKTNKMSCSLH-EECCFRCCFHGKC 26

RESULT 54

A30584
 Interleukin-1 beta precursor - rabbit
 N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating factor
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C;Accession: A27714; A30584; J00082; A32166
 R;Wori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
 Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
 A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating
 A;Reference number: A27714; MUID:88134238; PMID:2449207
 A;Accession: A27714
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-268 <MOR>
 A;Cross-references: UNIPROT:P14628
 R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C.
 J. Immunol. 142, 2299-2306, 1989
 A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during
 A;Reference number: A30584; MUID:89176242; PMID:2784458
 A;Accession: A30584
 A;Molecule type: mRNA
 A;Residues: 1-268 <CAN>
 A;Cross-references: GB:M26295; NID:G516632; PIDN:AAA1373.1; PID:G516633
 R;Young, P.R.; Sylvester, D.
 Protein Eng. 2, 545-551, 1989
 A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and beta
 A;Reference number: A94230; MUID:89315718; PMID:2787507
 A;Accession: J00082
 A;Molecule type: mRNA
 A;Residues: 1-268 <YOU>
 C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavage
 ved form of interleukin-1 beta, unlike interleukin 1-alpha, is inactive.
 C;Comment: Interleukin-1 beta precursor is less heavily myristoylated than interleukin-1
 C;Superfamily: interleukin-1
 C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
 F;117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match 30.7%; Score 49.5; DB 1; Length 268;
 Best Local Similarity 37.0%; Pred. No. 93;
 Matches 10; Conservative 3; Mismatches 7; Indels 7; Gaps 1;

QY 6 QKCFQHLDDCCSRK-----CNRFRNKC 25
 Db 33 KSCFQDLDCPDGEGIQLRISCPYNNK 59

RESULT 55

JE0120
 Glycoprotein A - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
 C;Accession: JE0120
 R;Haidaris, C.G.; Medzihradsky, O.F.; Gagliotti, F.; Simpson-haidaris, P.J.
 DNA Res. 5, 77-85, 1998
 A;Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A.
 A;Reference number: JE0120; MUID:98344138; PMID:9679195
 A;Accession: JE0120
 A;Molecule type: mRNA
 A;Residues: 1-1282 <HAI>
 A;Cross-references: GB:AF143102
 C;Comment: This protein is a surface antigen of pneumonia.

C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

C;Keywords: Glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.7%; Score 49.5; DB 2; Length 1282;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRF-NKC 26

Db 366 QCEVLEKCYFVGSSCKDKCKDKVNNKC 392

RESULT 56

T01055

hypothetical protein YUP8H12R.38 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01055

R;Theologias, A.; Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; Kwar
Oefner, P.; Davis, R.W.

submitted to the EMBL Data Library, May 1998

A;Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.

A;Reference number: Z14227

A;Accession: T01055

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1516 <THE>

A;Cross-references: UNIPROT:O64548; EMBL:AC002986; NID:g2494106; PID:g3152587; GSPDB:GN0

C;Genetics:

A;Gene: ATSP:YUP8H12R.38

A;Map position: 1

A;Introns: 59/2; 97/3; 185/1; 319/1; 379/1; 809/3; 908/3; 1001/3; 1044/3; 1111/3; 1159/2

Query Match

Best Local Similarity 30.7%; Score 49.5; DB 2; Length 1516;

Matches 7; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 3 IXNKCFOHLDCCSRKCNRFNKC 27

Db 543 VTQKLWKHWDSCAAPCS-YPRCL 566

RESULT 57

T16556

hypothetical protein K04C2.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C;Accession: T16556

R;Pauley, A.

submitted to the EMBL Data Library, April 1994

A;Description: The sequence of C. elegans cosmid K04C2.

A;Reference number: Z18534

A;Accession: T16556

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-194 <PAU>

A;Cross-references: EMBL:U00044; NID:g470346; PID:g470348; PIDN:AAA50676.1; CESP:K04C2.1

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:K04C2.1

A;Introns: 26/2; 85/3; 131/3

C;Superfamily: Caenorhabditis elegans hypothetical protein K04C2.1

Query Match

Best Local Similarity 30.4%; Score 49; DB 2; Length 194;

Matches 12; Conservative 6; Mismatches 8; Indels 10; Gaps 1;

QY 2 RIXNKCFOHLDCCS-----RKCNRNKC 27

Db 86 RIPNEILFEILENCKSTEPSTVLAARLSRRFNACM 121

A:Residues: 1-833 <SCH>
A:Cross-references: UNIPROT:O17102; EMBL:AF024499; PIDN:AAB70358.1; GSPDB:GN00020; CESP:
A:Experimental source: strain Bristol N2; clone F42G2
C:Genetics:
A:Gene: CESP:F42G2.6
A:Map position: 2
A:Introns: 317/1; 335/1; 362/3; 781/1

Query Match 30.4%; Score 49; DB 2; Length 833;
Best Local Similarity 26.9%; Pred. No. 2.2e+02;
Matches 7; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

Qy 2 RIXNQKCFQHLDDCCSRKCNRFKCV 27
Db 87 QVQNNCFQHLSPYSKFCFHYGHMI 112
:::|||||:::|::|

RESULT 61
A30889
Integrin beta chain precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 16-Aug-2004
C:Accession: A30889
R:Mackrell, A.J.; Blumberg, B.; Haynes, S.R.; Fessler, J.H.
Proc. Natl. Acad. Sci. U.S.A. 85, 2633-2637, 1988
A:Title: The lethal myospheroid gene of *Drosophila* encodes a membrane protein homologous
A:Reference number: A30889; MUID:88190122; PMID:3128792
A:Accession: A30889
A:Molecule type: mRNA
A:Residues: 1-846 <MAC>
A:Cross-references: UNIPROT:P11584; GB:J03251; NID:g157954; PIDN:AAA28714.1; PID:g157955
C:Genetics:
A:Gene: FlyBase:mys
A:Cross-references: FlyBase:FBgn0004657
C:Superfamily: Integrin beta chain; laminin-type EGF-like homology
C:Keywords: cell adhesion; cytoskeleton; transmembrane protein

Query Match 30.4%; Score 49; DB 2; Length 846;
Best Local Similarity 32.3%; Pred. No. 2.3e+02;
Matches 10; Conservative 6; Mismatches 11; Indels 4; Gaps 2;

Qy 1 CRIXNQKCF--QHLDDC--CSRKCNRFKCV 27
Db 669 CTVNDQGRFSGRHCCKPTCSGRCKQLKOCV 699
:::|||||:::|::|

RESULT 62
A40136
fibropellin Ia - sea urchin (*Strongylocentrotus purpuratus*)
N:Alternate names: epidermal growth factor homolog precursor
N:Contains: alternatively spliced fibropellin Ib (EGFI)
C:Species: *Strongylocentrotus purpuratus* (purple urchin)
C:Date: 13-May-1992 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A40136; B40136; C40136; A29316; A43131
R:Delgadillo-Reynos, M.G.; Rollo, D.R.; Hursh, D.A.; Raff, R.A.
J. Mol. Evol. 29, 314-327, 1989
A:Title: Structural analysis of the uEGF gene in the sea urchin *Strongylocentrotus purpuratus*
A:Reference number: A40136; MUID:90112459; PMID:2514273
A:Accession: A40136
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114
A:Cross-references: UNIPROT:P10079; GB:X17530; NID:g10225; PID:g667061
A:Accession: B40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 181-251,329-370,'R',372-408,'RA',411-441 <DE2>
A:Accession: C40136
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 'K',747-821,898-978 <DE3>
R:Hursh, D.A.; Andrews, M.E.; Raff, R.A.
Science 237, 1487-1490, 1987

A:Title: A sea urchin gene encodes a polypeptide homologous to epidermal growth factor.
A:Reference number: A29316; MUID:87319677; PMID:3498216
A:Accession: A29316
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 'S',280-481,786-1064 <HUP>
A:Cross-references: GB:M17421; NID:gl61474; PIDN:AAA30050.1; PID:g552260
R:Hunt, L.T.; Barker, W.C.
FASEB J. 3, 1760-1764, 1989
A:Title: Avidin-like domain in an epidermal growth factor homolog from a sea urchin.
A:Reference number: A43131; MUID:89196806; PMID:2784773
A:Contents: annotation
C:Comment: EGF homology repeats 10-17 are spliced out in the short form (fibropellin Ib)
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-1064/Product: fibropellin I #status predicted <FIB>
F:23-54/Domain: EGF homology <EG01>
F:57-175/Domain: C1r/C1s repeat homology <C1R>
F:180-211/Domain: EGF homology <EG02>
F:218-249/Domain: EGF homology <EG03>
F:256-287/Domain: EGF homology <EG04>
F:294-325/Domain: EGF homology <EG05>
F:332-363/Domain: EGF homology <EG06>
F:370-401/Domain: EGF homology <EG07>
F:408-439/Domain: EGF homology <EG08>
F:446-477/Domain: EGF homology <EG09>
F:484-515/Domain: EGF homology <EG10>
F:522-553/Domain: EGF homology <EG11>
F:560-591/Domain: EGF homology <EG12>
F:598-629/Domain: EGF homology <EG13>
F:636-667/Domain: EGF homology <EG14>
F:674-705/Domain: EGF homology <EG15>
F:712-743/Domain: EGF homology <EG16>
F:750-781/Domain: EGF homology <EG17>
F:788-819/Domain: EGF homology <EG18>
F:826-857/Domain: EGF homology <EG19>
F:864-895/Domain: EGF homology <EG20>
F:902-933/Domain: EGF homology <EG21>
F:936-1064/Region: avidin-like
F:23-34,28-43,45-54,62-88,180-191,185-200,202-211,218-229,223-238,240-249,256-267,261-271
57,451-466,468-477,484-495/Dsulfide bonds: #status predicted
F:489-504,506-515,522-533,527-542,544-553,560-571,565-580,582-591,598-609,603-618,620-621
08,810-819,826-837,831-846,848-857,864-875,869-884,886-895,902-913,907-922,924-933/Dsulf1

Query Match 30.4%; Score 49; DB 2; Length 1064;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 8 CFQHLDDCCSRKCNRFKCV 27
Db 439 CENNIDECASRPCQNGAVCV 458
:::|||||:::|::|

RESULT 63
A49175
Notch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: *Mus musculus* (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C:Accession: A49175; PH1570; S32113
R:Lardelli, M.; Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: UNIPROT:O35516; EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g28795
A:Experimental source: embryo
A:Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision between
C:Superfamily: Notch protein; ankyrin repeat homology; EGF homology

C;Accession: A00820
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00820
A;Molecule type: protein
A;Residues: 1-124 <VAN>
A;Cross-references: UNIPROT:P00675
A;Note: a second component of chinchilla ribonuclease has 32-Asp
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12.41.119/Active site: His, Lys, His #status predicted
F;26-84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 30.1%; Score 48.5; DB 1; Length 124;
Best Local Similarity 27.5%; Pred. No. 72;
Matches 11; Conservative 6; Mismatches 8; Indels 15; Gaps 2;

QY 1 CRXNOKCFQHLDDC-----HLDDC-----CSRKNRPNK 25
DB 65 CKNGQSNQYQSNWNIHIDCLRTLSKSNYPNCSYTSRENK 104

RESULT 69
JQ1739
N;Altername names: ORF6 protein
C;Species: shallot virus X
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: JQ1739
R;Kanyuka, K.V.; Vishnichenko, V.K.; Levay, K.E.; Kondrikov, D.V.; Ryabov, E.V.; Zavriv
J. Gen. Virol. 73, 2553-2560, 1992
A;Title: Nucleotide sequence of shallot virus X RNA reveals a 5'-proximal ciatron closed
A;Reference number: JQ1734; MUID:93019008; PMID:1339468
A;Accession: JQ1739
A;Molecule type: mRNA
A;Residues: 1-128 <KAN>
A;Cross-references: UNIPROT:Q04580
A;Experimental source: strain X

Query Match 30.1%; Score 48.5; DB 2; Length 128;
Best Local Similarity 34.6%; Pred. No. 74;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

QY 2 RIXNOKCFQHLDDCCS-RKCNRFNKC 26
DB 40 RLDDNPFQGTSCAKERRAKRYNRC 65

RESULT 70
G89152
protein C24B5.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G89152
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G89152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <STO>
A;Cross-references: UNIPROT:Q9TV01; GB:chr_V; PID:g4483503; GSFDB:GN00023; CESP:C24B5.5
C;Genetics:
A;Gene: C24B5.5
A;Map position: 5

Query Match 30.1%; Score 48.5; DB 2; Length 328;
Best Local Similarity 39.1%; Pred. No. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

Best Local Similarity 30.6%; Pred. No. 1.4e+02;
Matches 11; Conservative 7; Mismatches 9; Indels 9; Gaps 2;

QY 1 CRXNOKCFQHLDDC---CSRKC-----NRFNKCV 27
DB 170 CASONKTNQCANECNNQCANSCSPSSQTSYSKCV 205

RESULT 71
A45545
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A45545
R;Blackman, M.J.; Ling, I.T.; Nicholls, S.C.; Holder, A.A.
Mol. Biochem. Parasitol. 49, 29-33, 1991
A;Title: Proteolytic processing of the Plasmodium falciparum merozoite surface protein-1
A;Reference number: A45545; MUID:92131048; PMID:1775158
A;Accession: A45545
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <BLA>
A;Cross-references: UNIPROT:Q03999
A;Note: sequence extracted from NCBI backbone (NCBIN:77612, NCBI:P.77621)
C;Superfamily: major merozoite surface antigen
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat

Query Match 30.1%; Score 48.5; DB 2; Length 400;
Best Local Similarity 37.9%; Pred. No. 1.6e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 4 XNOKCFQHLDDCCSRKC-----NRFNKCV 27
DB 300 QNSGCFRHLDERECKCLLNYKQEGDKCV 328

RESULT 72
T09341
hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana
N;Alternate names: 3-hydroxy-3-methylglutaryl-coenzyme A synthase; protein T26M18.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09341; JC4567
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16650
A;Accession: T09341
A;Molecule type: DNA
A;Residues: 1-461 <BEV>
A;Cross-references: UNIPROT:P54873; EMBL:AL078606
A;Experimental source: cultivar Columbia; BAC clone T26M18
R;Montamat, F.; Guilloton, M.; Karst, F.; Delrot, S.
Gene 167, 197-201, 1995
A;Title: Isolation and characterization of a cDNA encoding Arabidopsis thaliana 3-hydroxy
A;Reference number: JC4567; MUID:96144274; PMID:8566777
A;Accession: JC4567
A;Molecule type: mRNA
A;Residues: 1-307 '341', 'N', '343-461' <MON>
A;Cross-references: EMBL:X83882; MID:G1143389; PIDN:CAA58763.1; PID:G1143390
C;Comment: This enzyme mediates the conversion of three acetyl-CoA molecules to one molec
ivity, and upakes amino acids.
C;Genetics:
A;Gene: ATSP:T26M18.30
A;Map position: 4
A;Introns: 21/3; 57/2; 101/3; 149/3; 202/3; 227/2; 252/3; 271/2; 300/3; 347/3; 397/3
C;Superfamily: hydroxymethylglutaryl-CoA synthase
C;Keywords: carbon-carbon lyase; coenzyme A; glycoprotein; oxo-acid-lyase
F;117/Active site: Cys (covalent substrate-binding) #status predicted
F;269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 48.5; DB 2; Length 461;
Best Local Similarity 39.1%; Pred. No. 1.7e+02;
Matches 9; Conservative 4; Mismatches 9; Indels 1; Gaps 1;

major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (std
RESULT 75
S05603
N;Alternate names: gp195 surface antigen
C;Species: Plasmodium falciparum
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S05603; S04850

A;Title: Merozoite surface protein sequence from the Camp strain of the human malaria parasite
A;Reference number: S06361; MUID:88143999; PMID:3278296
A;Accession: S06361
A;Molecule type: DNA
A;Residues: 1104-1726 <WEB2>
A;Cross-references: EMBL:X03831
C;Comment: The merozoite stages of different strains have strain-specific surface antigens
C;Superfamily: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The merozoite stage is the most abundant and is the stage that is most studied.
C;Keywords: glycoprotein; merozoite; surface antigen; tandem repeat
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1726/Product: major merozoite surface antigen #status predicted <SIG>
F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
F;757-765/Region: 3-residue repeats (T-E-E)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carboxy-terminal
Query Match 30.1%; Score 48.5; DB 1; Length 1726;
Best Local Similarity 37.9%; Pred. No. 4.1e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;
QY 4 XNOKCFQHLDDCCSRKNC-----NRFNKCV 27
Db 1626 ENSGCFRHLDERECKLLNRYKQEGDKCV 1654
RESULT 78
A45948
A;Title: Merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (strain 3D7)
A;Reference number: A45948
A;Accession: A45948
A;Molecule type: DNA
A;Residues: 1-1726 <CHA>
A;Cross-references: UNIPROT:Q25922; GB:M37213
C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
Query Match 30.1%; Score 48.5; DB 2; Length 1726;
Best Local Similarity 37.9%; Pred. No. 4.1e+02;
Matches 11; Conservative 4; Mismatches 9; Indels 5; Gaps 1;
QY 4 XNOKCFQHLDDCCSRKNC-----NRFNKCV 27
Db 1626 ENSGCFRHLDERECKLLNRYKQEGDKCV 1654
RESULT 79
S02007
A;Title: Primary structure of rabbit sperm protamine, the first protamine of its type with a unique structure
A;Reference number: S02007; MUID:89078594; PMID:3060372
A;Accession: S02007
A;Molecule type: protein
A;Residues: 1-49 <ANM>
A;Cross-references: UNIPROT:P10119
C;Superfamily: sperm histone
C;Keywords: DNA binding; nucleus
Query Match 29.8%; Score 48; DB 2; Length 49;
Best Local Similarity 34.6%; Pred. No. 45;
Matches 9; Conservative 5; Mismatches 10; Indels 2; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKNCNRNK 26
Db 14 CRRRRRCRRRRRCRRRCRRRCRRRC 37

RESULT 80

T26875
A;Title: hypothetical protein Y43F8C.16 - Caenorhabditis elegans
A;Reference number: T26875
A;Accession: T26875
A;Molecule type: DNA
A;Residues: 1-296 <WIL>
A;Cross-references: UNIPROT:Q9XWN5; EMBL:AL032637; PIDN:CAA21616.1; CESP:Y43F8C.16
A;Experimental source: clone Y43F8C
C;Genetics:
A;Gene: CESP:Y43F8C.16
A;Introns: 31/1; 53/2; 127/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y43F8C.16
Query Match 29.8%; Score 48; DB 2; Length 296;
Best Local Similarity 37.5%; Pred. No. 1.5e+02;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 3 IXNOKCFQHLDDCCSRKNCNRNK 26
Db 177 VIYHKCSTIHDDCRTYKNNFHC 200

RESULT 81

S64135
A;Title: hypothetical protein YGL124C - yeast (Saccharomyces cerevisiae)
A;Reference number: S64135
A;Accession: S64135
A;Molecule type: DNA
A;Residues: 1-644 <CER>
A;Cross-references: UNIPROT:P53129; EMBL:Z72646; NID:gl322684; PIDN:CAA96832.1; PID:e243;
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Title: Identification of a putative methyltetrahydrofolate reductase by sequence analysis
A;Reference number: S72026; MUID:97051592; PMID:8896269
A;Accession: S72027
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-644 <TIZ>
A;Cross-references: EMBL:X94106; NID:gl628448; PIDN:CAA63834.1; PID:e214776; PID:gl628450
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Gene: SGD:MON1
A;Cross-references: SGD:S0003092
A;Map position: 7L
A;Note: YGL124C

Query Match 29.8%; Score 48; DB 2; Length 644;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 FOHLDDCCSRKNCNR 22
Db 302 FENLDDCCSRKNCNR 315

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RESULT 82
A31246
neurogenic protein Delta precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Aug-2002
C:Accession: A31246
R:Kopcsynski, C.C.; Alton, A.K.; Fecht, K.; Kooh, P.J.; Muskavitch, M.A.T.
Genes Dev. 2, 1723-1735, 1988
A:Title: Delta, a Drosophila neurogenic gene, is transcriptionally complex and encodes a
A:Reference number: A31246; MUID:89196890; PMID:3149249
A:Accession: A31246
A:Molecule type: mRNA
A:Cross-references: GB:Y00222
C:Genetics:
A:Gene: FlyBase:DL
A:Cross-references: FlyBase:FBgn0000463
C:Superfamily: neurogenic protein delta; EGF homology
F:295-328/Domain: EGF homology <EGF1>
F:422-450/Domain: EGF homology <EGF1>
F:457-488/Domain: EGF homology <EGF>
F:533-564/Domain: EGF homology <EGF3>

Query Match 29.8%; Score 48; DB 2; Length 832;
Best Local Similarity 28.6%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 7 KCFQHLDDCCSRKCNRFNKCVCV 27
DB 449 RCETNIDDCGLGHQCENGGTCTI 469

RESULT 83
S19087
gene Delta protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S19087
R:Muskavitch, M.A.T.
submitted to the EMBL Data Library, June 1991
A:Reference number: S19087
A:Accession: S19087
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-833 <MUS>
A:Cross-references: UNIPROT:P10041; EMBL:Y00222
C:Genetics:
A:Gene: FlyBase:DL
A:Cross-references: FlyBase:FBgn0000463
C:Superfamily: neurogenic protein delta; EGF homology
F:335-371/Domain: EGF homology <EGF1>
F:378-415/Domain: EGF homology <EGF1>
F:457-488/Domain: EGF homology <EGF>
F:533-564/Domain: EGF homology <EGF3>

Query Match 29.8%; Score 48; DB 2; Length 833;
Best Local Similarity 28.6%; Pred. No. 2.9e+02;
Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 7 KCFQHLDDCCSRKCNRFNKCVCV 27
DB 449 RCETNIDDCGLGHQCENGGTCTI 469

RESULT 84
S0670
neurogenic repetitive locus delta protein precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: gene D1 protein
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: S0670; A26637
R:Vaessin, H.; Bremer, K.A.; Knust, E.; Campos-Ortega, J.A.
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EMBO J. 6, 3431-3440, 1987
A:Title: The neurogenic gene Delta of Drosophila melanogaster is expressed in neurogenic
A:Reference number: S0670
A:Accession: S0670
A:Molecule type: mRNA
A:Residues: 1-880 <VAE>
A:Cross-references: UNIPROT:P10041; EMBL:X06289; NID:G7852; PID:G7853
R:Knust, E.; Dietrich, U.; Tepass, U.; Bremer, K.A.; Weigel, D.; Vaessin, H.; Campos-Ortega, J.A.
EMBO J. 6, 761-766, 1987
A:Title: EGF homologous sequences encoded in the genome of Drosophila melanogaster, and
A:Reference number: A91081; MUID:87218537; PMID:3107986
A:Accession: A26637
A:Molecule type: mRNA
A:Residues: 422-436; 'ET', 439-458; 'A', 460-489; 'T', 491-621 <KNU>
A:Cross-references: GB:X05140; NID:G7851; PIDN:CAA28786.1; PID:G929563
C:Genetics:
A:Gene: Delta; DL
A:Cross-references: FlyBase:FBgn0000463
C:Superfamily: neurogenic protein delta; EGF homology
C:Keywords: transmembrane protein
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-88/Product: neurogenic repetitive locus delta protein #status predicted <MAT>
F:457-488/Domain: EGF homology <EGF1>
F:533-564/Domain: EGF homology <EGF2>

Query Match 29.8%; Score 48; DB 2; Length 880;
Best Local Similarity 28.6%; Pred. No. 3e+02;
Matches 6; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 7 KCFQHLDDCCSRKCNRFNKCVCV 27
DB 449 RCETNIDDCGLGHQCENGGTCTI 469

RESULT 85
S06434
homeotic protein lin-12 precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Aug-2004
C:Accession: S06434; A24769
R:Yochem, J.; Weston, K.; Greenwald, I.
Nature 335, 547-550, 1988
A:Title: The Caenorhabditis elegans lin-12 gene encodes a transmembrane protein with over
A:Reference number: S06434; MUID:88334747; PMID:3419531
A:Accession: S06434
A:Molecule type: DNA
A:Residues: 1-1429 <YOC>
A:Cross-references: UNIPROT:P14585; EMBL:M12069; NID:G156357; PIDN:AAA70191.1; PID:G156357
R:Greenwald, I.
Cell 43, 583-590, 1985
A:Reference number: A24769; MUID:86079540; PMID:3000611
A:Accession: A24769
A:Molecule type: DNA
A:Residues: 173-712 <GRE>
C:Genetics:
A:Introns: 50/2; 90/1; 109/1; 172/3; 545/1; 589/2; 632/2; 1273/3; 1389/3
C:Superfamily: ankyrin repeat homology; EGF homology
C:Keywords: glycoprotein; transmembrane protein
F:254-284/Domain: EGF homology <EGF1>
F:507-540/Domain: EGF homology <EGF2>
F:547-578/Domain: EGF homology <EGF2>
F:909-931/Domain: transmembrane #status predicted <TMM>
F:1093-1125/Domain: ankyrin repeat homology <AN1>
F:1206-1238/Domain: ankyrin repeat homology <AN2>
F:1240-1272/Domain: ankyrin repeat homology <AN3>

Query Match 29.8%; Score 48; DB 2; Length 1429;
Best Local Similarity 35.0%; Pred. No. 4.2e+02;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 8 CFFQHLDDCCSRKCNRFNKCVCV 27
DB 284 CQEGKDNVCVNNKCEAGSKCI 303
```

Query Match 29.8%; Score 48; DB 2; Length 3006;
Best Local Similarity 33.3%; Pred. NO. 6.8e+02;
Matches 9; Conservative 5; Mismatches 11; Indels 2; Gaps 1;

OY 1 CRXKNKCFQHLDDC--CSRKNRNNK 25
| : | : | : | : | : | : | : |
DB 1052 CKGKA SCTQKGDCCTKCAACDYNK 1078

RESULT 88

S02392
alpha-2-macroglobulin receptor precursor - human
N:Alternate names: CD91; LDL receptor-related protein 1; low density lipoprotein receptor
C:Species: Homo sapiens (man)
C>Date: 14-Aug-1998 #sequence revision 14-Aug-1998 #text_change 09-Jul-2004
C:Accession: S02392; S30027; I37998; A39210; S12538
R:Herz, J.; Hamann, U.; Rogne, S.; Mykleboost, O.; Gausepohl, H.; Stanley, K.K.
EMBO J. 7, 4119-4127, 1988
A>Title: Surface location and high affinity for calcium of a 500-kd liver membrane protei
A:Reference number: S02392; PMID:89210795; PMID:3266596
A:Accession: S02392
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-4544 <HER>
A:Cross-references: UNIPROT:Q07954; EMBL:X13916; NID:G34338; PIDN:CAA32112.1; PID:G34339
R:Kristensen, T.
submitted to the EMBL Data Library, October 1990
A:Reference number: S30027
A:Accession: S30027
A:Molecule type: mRNA
A:Residues: 3275-3864 <KRI>
A:Cross-references: EMBL:X55077
R:Herz, J.; Kowal, R.C.; Goldstein, J.L.; Brown, M.S.
EMBO J. 9, 1769-1776, 1990
A>Title: Proteolytic processing of the 600 kd low density lipoprotein receptor-related p
A:Reference number: S12538; PMID:90269210; PMID:2112085
A:Contents: annotation; site of proteolytic cleavage
R:Kutt, H.; Herz, J.; Stanley, K.K.
Biochim. Biophys. Acta 1009, 229-236, 1989
A>Title: Structure of the low-density lipoprotein receptor-related protein (LRP) promoter
A:Reference number: I37998; PMID:90089395; PMID:2597675
A:Accession: I37998
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: EMBL:X15424; NID:G34408; PIDN:CAA33464.1; PID:G34409
R:Strickland, D.K.; Ashcom, J.D.; Williams, S.; Buttgess, W.H.; Migliorini, M.; Argraves,
J. Biol. Chem. 265, 17401-17404, 1990
A>Title: Sequence identity between the alpha2-macroglobulin receptor and low density lip
A:Reference number: A39210; PMID:91009181; PMID:1698775

A;Residues: 150-166;234-238, 'X', 240-245, 'X', 247-252, 'G', 686-695;902-916;1096-1109, 'S', 174
A;Genetics:
A;Gene: GDB:LRP1, APR, LRP, A2MR
A;Cross-references: GDB:113694; OMIM:107770
A;Map position: 12q13.1-12q13.3
C;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associated protein (see PIR:A3875).
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
C;Keywords: beta-hydroxyasparagine; beta-hydroxyaspartic acid; calcium binding; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-3943/Product: alpha-2-macroglobulin receptor 515K chain #status predicted <515K>
F;27-64/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;72-108/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;115-148/Domain: EGF homology <EG1>
F;154-188/Domain: EGF homology <EG2>
F;198-239/Domain: LDL receptor YWTD-containing repeat homology <YW01>
F;240-281/Domain: LDL receptor YWTD-containing repeat homology <YW02>
F;292-334/Domain: LDL receptor YWTD-containing repeat homology <YW03>
F;335-378/Domain: LDL receptor YWTD-containing repeat homology <YW04>
F;379-420/Domain: LDL receptor YWTD-containing repeat homology <YW05>

F:479-520/Domain: EGF homology <EG3>
 F:572-614/Domain: LDL receptor WYTD-containing repeat homology <YW07>
 F:615-660/Domain: LDL receptor WYTD-containing repeat homology <YW08>
 F:661-711/Domain: LDL receptor WYTD-containing repeat homology <YW09>
 F:712-753/Domain: LDL receptor WYTD-containing repeat homology <YW10>
 F:754-800/Domain: LDL receptor WYTD-containing repeat homology <YW11>
 F:808-843/Domain: EGF homology <EG4>
 F:855-891/Domain: LDL receptor ligand-binding repeat homology <LDL3>
 F:896-932/Domain: LDL receptor ligand-binding repeat homology <LDL4>
 F:937-972/Domain: LDL receptor ligand-binding repeat homology <LDL5>
 F:977-1012/Domain: LDL receptor ligand-binding repeat homology <LDL6>
 F:1016-1052/Domain: LDL receptor ligand-binding repeat homology <LDL7>
 F:1063-1098/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:1105-1141/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:1146-1183/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:1186-1222/Domain: EGF homology <EG5>
 F:1228-1262/Domain: EGF homology <EG6>
 F:1270-1309/Domain: LDL receptor WYTD-containing repeat homology <YW12>
 F:1310-1356/Domain: LDL receptor WYTD-containing repeat homology <YW13>
 F:1357-1399/Domain: LDL receptor WYTD-containing repeat homology <YW14>
 F:1400-1446/Domain: LDL receptor WYTD-containing repeat homology <YW15>
 F:1447-1489/Domain: LDL receptor WYTD-containing repeat homology <YW16>
 F:1490-1532/Domain: LDL receptor WYTD-containing repeat homology <YW17>
 F:1541-1579/Domain: EGF homology <EG7>
 F:1584-1627/Domain: LDL receptor WYTD-containing repeat homology <YW18>
 F:1628-1670/Domain: LDL receptor WYTD-containing repeat homology <YW19>
 F:1671-1714/Domain: LDL receptor WYTD-containing repeat homology <YW20>
 F:1715-1754/Domain: LDL receptor WYTD-containing repeat homology <YW21>
 F:1755-1797/Domain: LDL receptor WYTD-containing repeat homology <YW22>
 F:1798-1847/Domain: LDL receptor WYTD-containing repeat homology <YW23>
 F:1851-1887/Domain: EGF homology <EG8>
 F:1935-1977/Domain: LDL receptor WYTD-containing repeat homology <YW24>
 F:1978-2020/Domain: LDL receptor WYTD-containing repeat homology <YW25>
 F:2021-2064/Domain: LDL receptor WYTD-containing repeat homology <YW26>
 F:2065-2106/Domain: LDL receptor WYTD-containing repeat homology <YW27>
 F:2107-2152/Domain: LDL receptor WYTD-containing repeat homology <YW28>
 F:2160-2195/Domain: EGF homology <EG9>
 F:2200-2242/Domain: LDL receptor WYTD-containing repeat homology <YW29>
 F:2254-2295/Domain: LDL receptor WYTD-containing repeat homology <YW30>
 F:2345-2389/Domain: LDL receptor WYTD-containing repeat homology <YW31>
 F:2390-2430/Domain: LDL receptor WYTD-containing repeat homology <YW32>
 F:2431-2474/Domain: LDL receptor WYTD-containing repeat homology <YW33>
 F:2483-2518/Domain: EGF homology <EG10>
 F:2525-2562/Domain: LDL receptor ligand-binding repeat homology <LDL8>
 F:2567-2601/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2606-2640/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2653-2689/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2697-2731/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2735-2770/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2775-2813/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2819-2854/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2859-2898/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2905-2940/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2945-2981/Domain: LDL receptor ligand-binding repeat homology <LDL9>
 F:2987-3022/Domain: EGF homology <EG11>
 F:3030-3069/Domain: LDL receptor WYTD-containing repeat homology <YW34>
 F:3070-3114/Domain: LDL receptor WYTD-containing repeat homology <YW35>
 F:3115-3157/Domain: LDL receptor WYTD-containing repeat homology <YW36>
 F:3158-3201/Domain: LDL receptor WYTD-containing repeat homology <YW37>
 F:3202-3242/Domain: LDL receptor WYTD-containing repeat homology <YW38>
 F:3243-3285/Domain: LDL receptor WYTD-containing repeat homology <YW39>
 F:3295-3331/Domain: EGF homology <EG13>
 F:3335-3370/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3375-3409/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3414-3449/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3454-3490/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3495-3532/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3537-3571/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3576-3610/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3614-3648/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3655-3691/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3696-3732/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:3742-3777/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F:3786-3823/Domain: EGF homology <EG14>
 F:3829-3861/Domain: EGF homology <EG15>
 F:3869-3912/Domain: LDL receptor WYTD-containing repeat homology <YW40>
 F:3913-3970/Domain: LDL receptor WYTD-containing repeat homology <YW41>
 F:3945-4545/Domain: alpha-2-macroglobulin receptor 85K chain #status predicted <85K>
 F:3945-4421/Domain: 85K chain extracellular #status predicted <EXT>
 F:3971-4013/Domain: LDL receptor WYTD-containing repeat homology <YW42>
 F:4014-4057/Domain: LDL receptor WYTD-containing repeat homology <YW43>
 F:4058-4100/Domain: LDL receptor WYTD-containing repeat homology <YW44>
 F:4101-4143/Domain: LDL receptor WYTD-containing repeat homology <YW45>
 F:4152-4183/Domain: EGF homology <EG16>
 F:4201-4232/Domain: EGF homology <EG17>
 F:4237-4268/Domain: EGF homology <EG18>
 F:4273-4304/Domain: EGF homology <EG19>
 F:4309-4340/Domain: EGF homology <EG20>
 F:4345-4375/Domain: EGF homology <EG21>
 F:4378-4409/Domain: EGF homology <EG22>
 F:4422-4445/Domain: Transmembrane #status predicted <TMW>
 F:4446-4545/Domain: intracellular #status predicted <INT>
 F:167,2999/Modified site: erythro-beta-hydroxyaspartic acid (Asn) #status predicted
 F:2959/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
 F:4076,4126,4279/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 48; DB 1; Length 4545;

Best Local Similarity 44.8%; Pred. No. 9e+02;
 Matches 13; Conservative 7; Mismatches 3; Indels 6; Gaps 4;

QY 1 CRXNKKCFQHLDDCCSRKC--NRPN-KC 26

Db 1222 CQIQSY-CAKHLK--CSQCDQKPSVKC 1247

RESULT 90

NRDEN

pancreatic ribonuclease [EC 3.1.27.5] - reindeer (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Rangifer tarandus (reindeer)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: B91418; A00812

R:Leijenaar-van den Berg, G.; Beintema, J.J.

FEBS Lett. 56, 101-107, 1975

A:Title: The amino acid sequences of reindeer, moose and fallow deer pancreatic ribonucle

A:Reference number: A91418; MUID:76003215; PMID:1157925

A:Accession: B91418

A:Molecule type: protein

A:Residues: 1-124 <LEI>

A:Cross-references: UNIPROT:P00666

C:Superfamily: pancreatic ribonuclease

C:Keywords: hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 29.5%; Score 47.5; DB 1; Length 124;

Best Local Similarity 25.0%; Pred. No. 94;

Matches 8; Conservative 7; Mismatches 12; Indels 5; Gaps 1;

QY 1 CRXNKKCFQ-----HLLDCCSRKCNRFNKC 27

Db 65 CKNGSQNCYQSNANMHTDCTGSSKYPNCV 96

RESULT 91

A39384

finger protein HPR4 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 08-Dec-2000

C:Accession: A39384

R:Belletrod, E.J.; Poncellet, D.A.; Lecocq, P.J.; Revelant, O.; Martial, J.A.

Proc. Natl. Acad. Sci. U.S.A. 88, 3608-3612, 1991

A:Title: The evolutionarily conserved Krueppel-associated box domain defines a subfamily

A:Reference number: A39384; MUID:91219421; PMID:2023909

A:Accession: A39384

A>Status: preliminary

Query Match 29.2%; Score 47; DB 2; Length 285;

```

Best Local Similarity 39.1%; Pred. No. 1.9e+02;
Matches 9; Conservative 6; Mismatches 6; Indels 2; Gaps 1;

QY 3 IXNKCFOHLD--DCCSRKCNRF 23
Db 147 IPPPKCFONTQGYKCCNRQLDQF 169

RESULT 97
AG3129
transcription regulator, Arac family agpT [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AG3129
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavain, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG3129
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KUR>
A:Cross-references: UNIPROT:Q8U6Z7; GB:AE008689; PIDN:AAU45453.1; PID:gl7743157; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: agpT
A:Map position: linear chromosome

Query Match 29.2%; Score 47; DB 2; Length 295;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 XNKCFOHLDCCSRKCN 21
Db 132 LQETVDHLAECCSLVN 149

RESULT 98
B98158
agpT protein (AF235048) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: B98158
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B98158
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KUR>
A:Cross-references: UNIPROT:Q8U6Z7; GB:AE007870; PIDN:AAK98788.1; PID:gi15158539; GSPDB:G
C:Genetics:
A:Gene: AGR_L_448
A:Map position: linear chromosome

Query Match 29.2%; Score 47; DB 2; Length 295;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 4 XNKCFOHLDCCSRKCN 21
Db 132 LQETVDHLAECCSLVN 149

RESULT 99
B71604
rRNA methylase (SpoU family) (OO, TP) PFB0855c - malaria parasite (Plasmodium falciparum

```

```

C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: B71604
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Perte, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: B71604
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-351 <GAR>
A:Cross-references: UNIPROT:O96263; GB:AE001421; GB:AE001362; NID:g3845293; PIDN:AACT7196
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0855c

Query Match 29.2%; Score 47; DB 2; Length 351;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 9; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

QY 1 CRXNKCFOHLDCCSRKCNRFN 24
Db 33 CKIKNQSCF--LNPCTHKVNDKRN 54

RESULT 100
T26564
hypothetical protein Y26D4A.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26564
R:White, S.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20234
A:Accession: T26564
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-365 <WIL>
A:Cross-references: UNIPROT:Q9U2Q2; EMBL:AL110478; NID:e1542139; PIDN:CAB54342.1; CESP:Y2
A:Experimental source: clone Y26D4A
C:Genetics:
A:Gene: CESP:Y26D4A.3
A:Introns: 30/1; 126/3; 174/2; 197/2; 223/1; 295/3; 335/2

Query Match 29.2%; Score 47; DB 2; Length 365;
Best Local Similarity 39.1%; Pred. No. 2.2e+02;
Matches 9; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 4 XNKCFOHLDCCSRKCNRFNKC 26
Db 284 SNQECQQRNQVVISRRARRINNC 306

Search completed: April 18, 2005, 20:38:46
Job time : 28.5 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 18, 2005, 20:00:51 ; Search time 117 Seconds
(without alignments)
118.172 Million cell updates/sec

Title: US-10-627-685a-26

Perfect score: 161

Sequence: 1 CR1XNOKCFOHLDCCSRKCNRFNKC 27

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	161	100.0	67	2	Q71KT2
2	161	100.0	72	1	CKX7 CONPU
3	78.5	48.8	67	2	Q6XE29
4	73	45.3	67	2	Q71KT1
5	71	44.1	67	2	Q71KS9
6	71	44.1	67	2	Q71KT0
7	71	44.1	72	1	CKOB CONST
8	68	42.2	38	1	POI MUSDO
9	66.5	41.3	1125	2	P92135
10	66	41.0	26	1	CKOC CONCT
11	63	39.1	2050	2	Q8IK03
12	62	38.5	46	1	HSPI_MYODA
13	61	37.9	29	1	CKOC CONMA
14	61	37.9	207	2	Q7PQD5
15	60	37.3	1685	2	Q9U4A2
16	59	36.6	638	2	Q7PM27
17	59	36.6	1410	2	Q20204
18	58	36.0	382	1	EFL9 MOUSE
19	58	36.0	383	1	BFL9 HUMAN
20	57	35.4	66	1	SCX1 OPICA
21	57	35.4	66	1	SCX2 OPICA
22	57	35.4	650	2	Q7Q0M5
23	57	35.4	752	2	Q42374
24	57	35.4	1245	2	Q80252
25	57	35.4	2524	1	NOTC XENLA
26	56.5	35.1	153	2	Q891K4
27	56.5	35.1	194	2	Q24821
28	56.5	35.1	372	2	Q8MU89
29	56.5	35.1	372	2	Q8MZT3
30	56.5	35.1	1292	2	Q24835
31	56.5	35.1	3467	2	Q81218

ALIGNMENTS

32	56	34.8	664	2	Q9IAT6
33	56	34.8	708	2	Q9LGM8
34	56	34.8	2703	1	NOTC DROME
35	55.5	34.5	25	1	CKOB CONMA
36	55.5	34.5	194	2	Q24822
37	55.5	34.5	372	2	Q8MZT1
38	55.5	34.5	372	2	Q8MZT2
39	55.5	34.5	1276	1	GILI ENTHI
40	55	34.2	33	1	SCXC SOMA
41	55	34.2	112	2	Q9PSU2
42	55	34.2	380	2	Q7XKS9
43	55	34.2	402	2	LHX5 XENLA
44	55	34.2	402	2	Q632R3
45	55	34.2	403	1	LHX1 XENLA
46	55	34.2	404	1	LHX1 HUMAN
47	55	34.2	406	1	LHX1 gall
48	55	34.2	406	1	LHX1 MESAU
49	55	34.2	406	1	LHX1_MOUSE
50	55	34.2	448	1	LHX1_RAT
51	55	34.2	448	2	Q26107
52	55	34.2	577	2	Q8HAD6
53	55	34.2	585	2	Q8OW06
54	55	34.2	587	2	Q8NBS4
55	55	34.2	589	1	DLI3_RAT
56	55	34.2	592	1	DLI3_MOUSE
57	55	34.2	618	1	DLI3 HUMAN
58	55	34.2	1620	2	Q812A6
59	55	34.2	5309	2	Q7RRT3
60	54.5	33.9	71	1	CKOA CONMA
61	54.5	33.9	74	2	Q646V4
62	54.5	33.9	74	2	Q646V5
63	54.5	33.9	74	2	Q646W1
64	54.5	33.9	247	2	O18052
65	54.5	33.9	252	2	Q97GL5
66	54.5	33.9	1382	2	O18720
67	54	33.5	73	1	CKOD CONCT
68	54	33.5	247	2	Q80LT7
69	54	33.5	405	1	LHX1 BRARE
70	54	33.5	552	2	O45117
71	54	33.5	911	2	Q68KF8
72	54	33.5	1372	2	P91526
73	54	33.5	1515	2	Q9DE37
74	53.5	33.2	84	1	HSPC_ELECI
75	53.5	33.2	476	2	Q693N8
76	53.5	33.2	572	1	NH25 CAEEL
77	53	32.9	33	1	ITXA_PANIM
78	53	32.9	85	2	Q8XKX8
79	53	32.9	191	2	Q6LZL1
80	53	32.9	225	2	Q7XZ30
81	53	32.9	234	2	Q86152
82	53	32.9	277	2	O23297
83	53	32.9	283	2	Q8L467
84	53	32.9	421	2	O44635
85	53	32.9	1286	2	Q7QCT2
86	53	32.9	2531	2	O16004
87	53	32.9	2556	1	NTC1 HUMAN
88	52.5	32.6	47	1	HSPI_PLETO
89	52.5	32.6	74	2	Q646U5
90	52.5	32.6	74	2	Q646U7
91	52.5	32.6	92	2	Q6PYV0
92	52.5	32.6	474	2	P93773
93	52.5	32.6	764	2	Q6K5W7
94	52.5	32.6	1285	1	SL17 ENTHI
95	52	32.3	354	2	Q8XV21
96	52	32.3	487	2	Q8MSX5
97	52	32.3	539	1	WNT4_DROME
98	52	32.3	778	2	Q91BG4
99	52	32.3	1069	2	Q96VI2
100	52	32.3	2139	1	CRB_DROME

Q9IAT6	brachydanio
Q9LGM8	oryza sativ
P07207	drosophila
P05485	conus magus
Q24822	entamoeba h
Q8MZ11	entamoeba h
Q8MZ22	entamoeba h
P32022	entamoeba h
P60254	scorpio mau
Q9PSU2	xenopus lae
O7XKS9	oryza sativ
P37137	xenopus lae
Q632R3	xenopus lae
P29674	xenopus lae
P48742	homo sapien
P53411	gallus gall
P63108	mesocricetu
P63006	mus musculu
P63007	rattus norv
Q26107	plasmodium
Q8HAD6	salmonella
Q8OW06	mus musculu
Q8NBS4	homo sapien
Q88671	rattus norv
O88516	mus musculu
Q9NY17	homo sapien
Q812A6	plasmodium
Q7RRT3	plasmodium
P05484	conus magus
Q646V4	phytophthor
Q646V5	phytophthor
Q646W1	phytophthor
O18052	caenorhabdi
Q97GL5	clostridium
O18720	entamoeba d
P58920	conus catus
Q80LT7	adoxophyes
Q90476	brachydanio
O45117	chironomus
Q68KF8	xenopus lae
P91526	caenorhabdi
Q9DE37	brachydanio
P83183	eledone cir
Q693N8	taxus x med
Q19345	caenorhabdi
P59868	pandinus im
Q8XKX8	clostridium
Q6LZL1	methanococc
Q7XZ30	griffithsia
Q86152	dictyosteli
O23297	arabidopsis
Q8L467	arabidopsis
O44635	caenorhabdi
Q7QCT2	anopheles g
O16004	lytechinus
P46531	homo sapien
Q8WZ02	plecotus to
Q646U5	phytophthor
Q646U7	phytophthor
Q6PYV0	schtstoma
P93773	pinus sylve
Q6K5W7	oryza sativ
P23022	entamoeba h
Q9XV21	caenorhabdi
Q8MSX5	drosophila
P40589	drosophila
Q91BG4	xenopus lae
Q96VI2	pneumocysti
P10040	drosophila

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RESULT 1
QY 071KT2
AC Q71KT2 PRELIMINARY; PRT; 67 AA.
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMELrel. 27, Last annotation update)
OS Four-loop conotoxin preproprotein (Fragment).
OC Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480312; AAQ05864.1; -
DR HSP; P56633; IAV3.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41 67 four-loop conotoxin.
SQ SEQUENCE 67 AA; 7712 MW; E7E77CC61873E1DB CRC64;

Query Match 100.0%; Score 161; DB 2; Length 67;
Best Local Similarity 96.3%; Pred. No. 1.4e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNKC 27
Db 41 CRIPNQKCFQHLDDCCSRKCNRFNKC 57

RESULT 2
CKX7_CONPU STANDARD; PRT; 72 AA.
ID AC P56633;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Kappa-conotoxin PVIIA precursor (Fin-popping peptide).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A., SYNTHESIS, AND MASS SPECTROMETRY.
RX MEDLINE=98079023; PubMed=9417043; DOI=10.1074/jbc.273.1.33;
RA Shon K.-J., Stocker M., Terlau H., Stuehmer W., Jacobsen R.B.,
RA Walker C.S., Grille M.M., Watkins M., Hillyard D.R., Gray W.R.,
RA Olivera B.M.;
RT "Kappa-conotoxin PVIIA is a peptide inhibiting the shaker K+
channel.";
RL J. Biol. Chem. 273:33-38(1998).
RN [2]
RP SEQUENCE OF 46-72, AND SYNTHESIS.
RX MEDLINE=22068471; PubMed=12074021; DOI=10.1038/381148a0;
RA Terlau H., Shon K.-J., Grille M.M., Stocker M., Stuehmer W.,
RA Olivera B.M.;
RT "Strategy for rapid immobilization of prey by a fish-hunting marine
snail.";
RL Nature 381:148-151(1996).
RN [3]
RP STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98104087; PubMed=9438859; DOI=10.1016/S0969-2126(97)00307-9;
RA Scanlon M.J., Naranjo D., Thomas L., Alewood P.F., Lewis R.J.,

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RA Craik D.J.;
RT "Solution structure and proposed binding mechanism of a novel
potassium channel toxin kappa-conotoxin PVIIA.";
RL Structure 5:1585-1597(1997).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98217295; PubMed=9548922; DOI=10.1021/bi9730341;
RA Savarin P., Guennegues M., Gilquin B., Lamthanh H., Gasparini S.,
RA Zinn-Justin S., Menez A.;
RT "Three-dimensional structure of kappa-conotoxin PVIIA, a novel
potassium channel-blocking toxin from cone snails.";
RL Biochemistry 37:5407-5416(1998).
RN [5]
RP MUTAGENESIS OF ARG-47; ILE-48; PRO-49; ASN-50; GLN-51; LYS-52; PHE-54;
PHE-54; GLN-55; HIS-56; LEU-57; ASP-58; ASP-59; SER-62; ARG-63;
LYS-64; ARG-67; PHE-68; ASN-69 AND LYS-70.
RX MEDLINE=20387358; PubMed=10818087; DOI=10.1074/jbc.C900990199;
RA Jacobsen R.B., Koch E.D., Lange-Malecki B., Stocker M., Verhey J.,
RA Van Wagoner R.M., Vyazovkina A., Olivera B.M., Terlau H.;
RT "Single amino acid substitutions in kappa-conotoxin PVIIA disrupt
interaction with the shaker K+ channel.";
RL J. Biol. Chem. 275:24639-24644(2000).
RN [6]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=99329121; PubMed=10398696;
RA Terlau H., Boccaccio A., Olivera B.M., Conti F.;
RT "The block of Shaker K+ channels by kappa-conotoxin PVIIA is state
dependent.";
RL J. Gen. Physiol. 114:125-140(1999).
RN [7]
RP MODEL OF THE SHAKER-PVIIA INTERACTION.
RX MEDLINE=21678121; PubMed=11820396;
RA Moran O.;
RT "Molecular simulation of the interaction of kappa-conotoxin-PVIIA with
the shaker potassium channel pore.";
RL Eur. Biophys. J. 30:528-536(2001).
RN [8]
RP BLOCKADE OF SHAKER CHANNEL BY PVIIA.
RX MEDLINE=22017751; PubMed=12023223;
RA Naranjo D.;
RT "Inhibition of single Shaker K channels by kappa-conotoxin-PVIIA.";
RL Biophys. J. 82:3003-3011(2002).
CC -!- FUNCTION: Kappa-conotoxins bind and inhibit voltage-sensitive
potassium channels. The rat brain voltage-gated potassium channel
protein Kv1.1 is resistant to this toxin, but the voltage-gated
potassium channel protein Shaker (Drosophila) is sensitive. The
interaction site between the Shaker channel and this toxin is
within the S5-S6 loop of the Shaker channel. In fish, this toxin
induces hyperactivity, followed by continuous contraction and
extension of major fins, without immobilization or death.
Injection of this peptide together with the delta-conotoxin PVIA
causes the sudden tetanus of prey (STOP) syndrome, which is a
single, lethal "fin-pop" in envenomated fish. In mice, induces
hyperactivity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=3268.4; METHOD=FAB; RANGE=46-72; NOTE=Ref.1.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Kappa-type
family.
CC -!- CAUTION: Because analogs resulting from mutagenesis of Hyp-49, Asn-
50, Leu-57 and Asp-59 gave very low yields upon folding, the
results of mutagenesis on these residues should be interpreted
with caution.
CC PIR; A58997; A58997.
CC PDB; 1AV3; NMR; @=1-27.
CC PDB; 1KCP; NMR; @=1-27.
CC InterPro; IPR004214; Conotoxin.
CC Pfam; PF02950; Conotoxin; 1.
CC 3D-structure; Direct protein sequencing; Hydroxylation;
KW Ionic channel inhibitor; Neurotoxin; Potassium channel inhibitor;
KW Signal; Toxin.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 45

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FT PEPTIDE 46 72 Kappa-conotoxin PVIIA.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 71
FT MOD_RES 49 49
FT MUTAGEN 47 47
FT MUTAGEN 48 48
FT MUTAGEN 49 49
FT MUTAGEN 50 50
FT MUTAGEN 51 51
FT MUTAGEN 52 52
FT MUTAGEN 54 54
FT MUTAGEN 54 54
FT MUTAGEN 55 55
FT MUTAGEN 56 56
FT MUTAGEN 57 57
FT MUTAGEN 58 58
FT MUTAGEN 59 59
FT MUTAGEN 62 62
FT MUTAGEN 63 63
FT MUTAGEN 64 64
FT MUTAGEN 67 67
FT MUTAGEN 68 68
FT MUTAGEN 69 69
FT MUTAGEN 70 70
FT STRAND 47 47
FT TURN 49 50
FT TURN 52 52
FT HELIX 55 57
FT STRAND 60 60
FT STRAND 65 65
FT TURN 67 68
FT STRAND 70 72
SQ SEQUENCE 72 AA; 8317 MW; 53BFAF79BE751C16 CRC64;

Query Match 100.0%; Score 161; DB 1; Length 72;
Best Local Similarity 96.3%; Pred. No. 1.5e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFKVCV 27
Db 46 CRIPNOKCFQHLDDCCSRKCNRFKVCV 72

RESULT 3
Q6XE29 PRELIMINARY; PRT; 67 AA.
AC Q6XE29;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus emineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY236862; AAF75888.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
FT CHAIN 41 67
SQ SEQUENCE 67 AA; 7575 MW; EBD557FB2EE9134 CRC64;

Query Match 48.8%; Score 78.5; DB 2; Length 67;
Best Local Similarity 46.2%; Pred. No. 0.019;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

FT PEPTIDE 46 72 Kappa-conotoxin PVIIA.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 71
FT MOD_RES 49 49
FT MUTAGEN 47 47
FT MUTAGEN 48 48
FT MUTAGEN 49 49
FT MUTAGEN 50 50
FT MUTAGEN 51 51
FT MUTAGEN 52 52
FT MUTAGEN 54 54
FT MUTAGEN 54 54
FT MUTAGEN 55 55
FT MUTAGEN 56 56
FT MUTAGEN 57 57
FT MUTAGEN 58 58
FT MUTAGEN 59 59
FT MUTAGEN 62 62
FT MUTAGEN 63 63
FT MUTAGEN 64 64
FT MUTAGEN 67 67
FT MUTAGEN 68 68
FT MUTAGEN 69 69
FT MUTAGEN 70 70
FT STRAND 47 47
FT TURN 49 50
FT TURN 52 52
FT HELIX 55 57
FT STRAND 60 60
FT STRAND 65 65
FT TURN 67 68
FT STRAND 70 72
SQ SEQUENCE 72 AA; 8317 MW; 53BFAF79BE751C16 CRC64;

Query Match 100.0%; Score 161; DB 1; Length 72;
Best Local Similarity 96.3%; Pred. No. 1.5e-12;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKCNRFKVCV 27
Db 46 CRIPNOKCFQHLDDCCSRKCNRFKVCV 72

RESULT 3
Q6XE29 PRELIMINARY; PRT; 67 AA.
AC Q6XE29;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus emineus (Atlantic fish-hunting cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=55423;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY236862; AAF75888.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
FT CHAIN 41 67
SQ SEQUENCE 67 AA; 7575 MW; EBD557FB2EE9134 CRC64;

Query Match 48.8%; Score 78.5; DB 2; Length 67;
Best Local Similarity 46.2%; Pred. No. 0.019;
Matches 12; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 CRXNQKCFQHLDDCCSRKCNRFKNC 26
Db 42 CKPKGRKCFPHQKDCCKTKCTR-SKC 66

RESULT 4
Q71KTL PRELIMINARY; PRT; 67 AA.
AC Q71KTL;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480313; AAQ05865.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
FT CHAIN 41 67
SQ SEQUENCE 67 AA; 7358 MW; E311E06BB6AF702E CRC64;

Query Match 45.3%; Score 73; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.088;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKNC 20
Db 42 CKTPGRKCFPHQKDCGGRAC 61

RESULT 5
Q71KS9 PRELIMINARY; PRT; 67 AA.
AC Q71KS9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480313; AAQ05867.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1 1
FT CHAIN 41 67
SQ SEQUENCE 67 AA; 7488 MW; 1B483B1BB6AF7755 CRC64;

Query Match 44.1%; Score 71; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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OY 1 CRXNKKCFQHLDDCCSRKC 20
Db 42 CKTKGKCFPHQKDCGGRAC 61

RESULT 6
Q71KTO PRELIMINARY; PRT; 67 AA.
AC Q71KTO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Four-loop conotoxin preproprotein (Fragment).
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE FROM N.A.
RA Duda T.F. Jr., Palumbi S.R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF480314; AAQ05866.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
FT CHAIN 41 67 four-loop conotoxin.
SQ SEQUENCE 67 AA; 7529 MW; 33E83B1EB6AF7435 CRC64;

Query Match 44.1%; Score 71; DB 2; Length 67;
Best Local Similarity 50.0%; Pred. No. 0.15;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 CRXNKKCFQHLDDCCSRKC 20
Db 42 CKTKGKCFPHQKDCGGRAC 61

RESULT 7
CXOB CONST STANDARD; PRT; 72 AA.
AC P28881; Q9UB25;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxin SVIB precursor (SNX-183).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu B.-S., Yu F., Zhao D., Huang P.-T., Huang C.-F.;
RL "Conopeptides from Conus striatus and Conus textile by cDNA cloning.";
RN Peptides 20:1139-1144 (1999).
[2]
RP SEQUENCE OF 46-71, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=93003172; PubMed=1390774;
RA Ramilo C., Zafaralla G.C., Nadasdi L., Hammerland L.G., Yoshikami D.,
RA Gray W.R., Kristipati R., Ramachandran J., Miljanich G., Olivera B.M.,
RA Cruz L.J.;
RT "Novel alpha" and omega-conotoxins from Conus striatus venom.";
RL Biochemistry 31:9319-9326 (1992).
[3]
RP STRUCTURE BY NMR.
RX MEDLINE=97070382; PubMed=8913308; DOI=10.1006/jmbi.1996.0576;

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RA Nielsen K.J., Thomas L., Lewis R.J., Alewood P.F., Craik D.J.;
RT "A consensus structure for omega-conotoxins with different
RT selectivities for voltage-sensitive calcium channel subtypes:
RT comparison of MWIIA, SVIB and SNX-202.";
RL J. Mol. Biol. 263:297-310 (1996).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC). This toxin
CC blocks N-, P-, and Q-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AF146346; AAD31906.1; -.
DR PIR; C44379; C44379.
DR PDB; 1MWJ; NMR; @=46-72.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
KW 3D-structure; Amidation; Calcium channel inhibitor;
KW Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
KW Presynaptic neurotoxin; Signal; Toxin.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 45
FT PEPTIDE 46 71 Omega-conotoxin SVIB.
FT DISULFID 46 61
FT DISULFID 53 65
FT DISULFID 60 71
FT MOD_RES 71 71
FT SEQUENCE 72 AA; 7741 MW; 1F753546AAD39908 CRC64;

Query Match 44.1%; Score 71; DB 1; Length 72;
Best Local Similarity 42.3%; Pred. No. 0.16;
Matches 11; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

OY 1 CRXNKKCFQHLDDCCSRKCNFNKC 26
Db 46 CLKXGQSCRKTSYDCCSGCSGRSGKC 71

RESULT 8
POI_MUSDO STANDARD; PRT; 38 AA.
AC P81765;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tyrosinase inhibitor (Phenol oxidase inhibitor) (Phenoloxidase
DE inhibitor) (POI).
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
OC Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND MASS SPECTROMETRY.
RC TISSUE=Hemolymph; PubMed=7708756;
RX MEDLINE=9524060;
RA Daquing A.C., Nakamura S., Takao T., Shimonishi Y., Tsukamoto T.;
RT "Primary structure of a potent endogenous dopa-containing inhibitor of
RT phenol oxidase from Musca domestica.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2964-2968 (1995).
[2]
RP SEQUENCE OF 6-9, CHARACTERIZATION, AND DEVELOPMENTAL STAGE.
RC TISSUE=Hemolymph;

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RX MEDLINE=92231987; PubMed=1567460;
RA Tsukamoto T., Ichimaru Y., Kanegae N., Watanabe K., Yamaura I.,
RA Katsura Y., Funatsu M.;
RT "Identification and isolation of endogenous insect phenoloxidase
RT inhibitors.";
RL Biochem. Biophys. Res. Commun. 184:86-92(1992).
RN [3]
RP SYNTHESIS, AND DISULFIDE BONDS.
RX MEDLINE=99152007; PubMed=10026302; DOI=10.1021/bi9819834;
RA Daquinag A.C., Sato T., Koda H., Takao T., Fukuda M., Shimomishi Y.,
RA Tsukamoto T.;
RT "A novel endogenous inhibitor of phenoloxidase from Musca domestica
RT has a cysteine motif commonly found in snail and spider toxins.";
RL Biochemistry 38:2179-2188(1999).
CC -1- FUNCTION: Potent reversible, competitive inhibitor of tyrosinase
CC (phenol oxidase) in the nanomolar range.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: POI activity increases throughout
CC pupariation, and is highest in final instar pupae. No activity in
CC newly emerged adults.
CC -1- MASS SPECTROMETRY: MW=4213.1; MW_ERR=0.2; METHOD=Electrospray;
CC RANGE=1-38; NOTE=Ref.1.
KW Direct protein sequencing; Hydroxylation.
FT DISULFID 11 25
FT DISULFID 18 29
FT DISULFID 24 36
FT MOD_RES 32 32 3',4'-dihydroxyphenylalanine.
SQ SEQUENCE 38 AA; 4204 MW; E597BE0BF286792 CRC64;

Query Match 42.2%; Score 68; DB 1; Length 38;
Best Local Similarity 39.3%; Pred. No. 0.22;
Matches 11; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

QY 1 CRIXNOKCFQHLDDCCSRKCNRF-NKCV 27
DB 11 CLANGSKCYSH-DVCCTRCHNYAKCV 37

RESULT 9
P92135 PRELIMINARY; PRT; 1125 AA.
ID P92135
AC P92135;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gal/GalNAc lectin heavy subunit (Fragment).
GN Name=hg12;
OS Entamoeba dispar.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=46681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAW 760;
RA Dodson J.M., Clark C.G., Lockhart L.A., Leo B.M., Schroeder J.W.,
RA Mann B.J.;
RL EMBL: U95822; AAB50229.1; -.
DR HSSP: P60045; IMF4.
DR GO: GO:0005529; F:sugar binding; IEA.
DR InterPro: IPR006209; EGF_like.
DR PROSITE: PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
FT NON_TER 1 1
FT NON_TER 1125 1125
SQ SEQUENCE 1125 AA; 126050 MW; 8DA832DE48A717C4 CRC64;

Query Match 41.3%; Score 66.5; DB 2; Length 1125;
Best Local Similarity 44.8%; Pred. No. 6.7;
Matches 13; Conservative 4; Mismatches 9; Indels 3; Gaps 2;

QY 1 CRIXNOKCFQHLDDCCSRK--CNRFN-KC 26
| : : : ||||| | |||

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Db 688 CSMGTDNVIRYHDDCCSRKSCQGNFNGKC 716

RESULT 10
CXOC_CONCT STANDARD; PRT; 26 AA.
ID P58919;
AC P58919;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin CVIC.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes.";
RL J. Biol. Chem. 275:35335-35344(2000).
CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC) (By
CC similarity). This toxin blocks N-, P-, and Q-type calcium
CC channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
DR HSSP: P05484; LDW4.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT DISULFID 1 16 By similarity.
FT DISULFID 8 20 By similarity.
FT DISULFID 15 26 By similarity.
FT MOD_RES 26 26 Cysteine amide.
SQ SEQUENCE 26 AA; 2790 MW; 56EFC382335C4A8B CRC64;

Query Match 41.0%; Score 66; DB 1; Length 26;
Best Local Similarity 38.5%; Pred. No. 0.28;
Matches 10; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 CRIXNOKCFQHLDDCCSRKCNRFNKC 26
| : : : ||||| | |||
DB 1 CRKGQSCSKLMYDCCGSCSRRGKC 26

RESULT 11
Q81K03 PRELIMINARY; PRT; 2050 AA.
ID Q81K03
AC Q81K03;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PF10_0037;
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2255705; PubMed=12368864; DOI=10.1038/nature01097;
RA Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
RA Carlton J.M., Paine A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
RA Chan M.S., Nene V., Shallow S.J., Suh B., Peterson J., Angiuoli S.,
RA Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
RA Martin D.M., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

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RA McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
 RA Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
 RA Fraser C.M., Barrell B.,
 RT "Genome sequence of the human malaria parasite Plasmodium
 RT falciparum"; -
 RL Nature 419:498-511(2002).
 DR EMBL; AE014829; AAN35235.1; -
 DR HSSP; Q93IC2; 1MWX.
 KW Hypothetical protein.
 SQ SEQUENCE 2050 AA; 241382 MW; 0A0586A5B42A3B8C CRC64;

Query Match 39.1%; Score 63; DB 2; Length 2050;
 Best Local Similarity 40.0%; Pred. No. 30;
 Matches 12; Conservative 8; Mismatches 6; Indels 4; Gaps 2;
 QY 1 CRXNKKCFQH---LDDCCSRKCNFN-KC 26
 DB 574 CNKLNKCTQECNKLNKCTQECNKLNK 603

RESULT 12
 HSPI_MYODA
 ID HSPI_MYODA STANDARD; PRT; 46 AA.
 AC Q8WNY8;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Sperm protamine P1.
 GN Name=PRM1;
 OS Myotis daubentonii (Daubenton's bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Vespertilionidae;
 OC Myotis.
 OX NCBI_TaxID=98922;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21881971; PubMed=11884158; DOI=10.1006/mpev.2001.1051;
 RA Van Den Bussche R.A., Hofer S.R., Hansen E.W.;
 RT "Characterization and phylogenetic utility of the mammalian protamine
 RT P1 gene";
 RL Mol. Phylogenet. Evol. 22:333-341(2002).
 CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact
 CC sperm DNA into a highly condensed, stable and inactive complex (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- TISSUE SPECIFICITY: Testis.
 CC -1- SIMILARITY: Belongs to the protamine P1 family.

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 CC -----
 DR EMBL; AF435946; AAL3580.1; -
 DR InterPro; IPR000221; Protamine_P1.
 DR Pfam; PF00260; Protamine_P1; 1.
 DR PROSITE; PS00048; PROTAMINE_P1; FALSE_NEG.
 KW Chromosomal protein; DNA condensation; DNA-binding; Nuclear protein;
 KW Nucleosome core; Spermatogenesis; Testis.
 FT INIT MET 0 0 By similarity.
 SQ SEQUENCE 46 AA; 6397 MW; CDBDD686E6A7BED CRC64;

Query Match 38.5%; Score 62; DB 1; Length 46;
 Best Local Similarity 28.1%; Pred. No. 1.4;
 Matches 9; Conservative 9; Mismatches 8; Indels 6; Gaps 1;

QY 1 CRXNKKCFQHLDCCSRK-----CNRFNK 26
 DB 12 CSRNRRCVRRRCRRRRRRRVCCRYSRC 43

RESULT 13
 CXOC_CONMA STANDARD; PRT; 29 AA.
 ID CXOC_CONMA
 AC P37300;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 25-OCT-1994 (Rel. 30, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Omega-conotoxin MVIIc precursor (SNX-230) (Fragment).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE FROM N.A., AND SYNTHESIS.
 RX MEDLINE=92337922; PubMed=1352986; DOI=10.1016/0896-6273(92)90221-X;
 RA Hillyard D.R., Monje V.D., Mintz I.M., Bean B.P., Nadasdi L.,
 RA Ramachandran J., Miljanich G.P., Azimi-Zoonooz A., McIntosh J.M.,
 RA Cruz L.J., Imperial J.S., Olivera B.M.;
 RT "A new Conus peptide ligand for mammalian presynaptic Ca2+ channels.";
 RL Neuron 9:69-77(1992).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95248539; PubMed=7731037;
 RA Farr-Jones S., Miljanich G.P., Nadasdi L., Ramachandran J.,
 RA Basus V.J.;
 RT "Solution structure of omega-conotoxin MVIIc, a high affinity ligand
 RT of P-type calcium channels, using 1H NMR spectroscopy and complete
 RT relaxation matrix analysis.";
 RL J. Mol. Biol. 248:106-124(1995).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE=99303703; PubMed=10373375; DOI=10.1006/jmbi.1999.2817;
 RA Nielsen K.J., Adams D., Thomas L., Bond T., Alewood P.F., Craik D.J.,
 RA Lewis R.J.;
 RT "Structure-activity relationships of omega-conotoxins MVIIA, MVIIc and
 RT 14 loop splice hybrids at N and P/Q-type calcium channels.";
 RL J. Mol. Biol. 289:1405-1421(1999).
 RN [4]
 RP MUTAGENESIS OF TYR-15.
 RX MEDLINE=95408251; PubMed=7677735;
 RA Kim J.I., Takahashi M., Martin-Moutot N., Seagar M.J., Ohtake A.,
 RA Sato K.;
 RT "Tyrl3 is essential for the binding of omega-conotoxin MVIIc to the
 RT P/Q-type calcium channel.";
 RL Biochem. Biophys. Res. Commun. 214:305-309(1995).
 CC -1- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
 CC and block voltage-sensitive calcium channels (VSCC). This toxin
 CC blocks N-type calcium channels as well as types of high-threshold
 CC voltage-gated calcium channels resistant to both dihydropyridines
 CC and omega-conotoxin GVIA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
 CC family.
 CC -----
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 CC -----
 DR EMBL; S40826; AAB22674.1; -
 DR PIR; JH0699; JH0699.
 DR PDB; 1CNN; NMR; A=3-29.
 DR PDB; 1OMN; NMR; @=3-29.
 KW 3D-structure; Amidation; Calcium channel inhibitor; Hydroxylation;
 KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
 FT NON_TER 1

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FT PROPEP      <1 2      Omega-conotoxin MVIIc.
FT PEPTIDE     3 28      Essential for calcium channel binding.
FT BINDING     15 15
FT DISULFID    3 18
FT DISULFID    10 22
FT DISULFID    17 28
FT MOD_RES     9 9      Hydroxyproline (Probable).
FT MOD_RES     28 28      Cysteine amide (G-29 provides amide
                          Y->A: High decrease in binding.
FT MUTAGEN     15 15
FT TURN        6 7
FT STRAND      9 9
FT HELIX       12 14
FT TURN       24 25
FT STRAND     27 27
SQ SEQUENCE    29 AA; 3071 MW; AC7A68948474728A CRC64;

Query Match      37.9%; Score 61; DB 1; Length 29;
Best Local Similarity 38.5%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 10; Conservative 4; Mismatches 12;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNK 26
   | : : : : | | | | |
Db 3 CRKGAPCRKTYWDCSGSGRGKC 28

RESULT 14
ID Q7PD5 PRELIMINARY; PRT; 207 AA.
AC Q7PD5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000015215 (Fragment).
GN Name=ENSANGG0000012726;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100897; EAA08999.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008200; F:ion channel inhibitor activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 2.
FT NON_TER 207 207
SQ SEQUENCE 207 AA; 22432 MW; 2F4552091F91FBE8 CRC64;

Query Match      37.9%; Score 61; DB 2; Length 207;
Best Local Similarity 46.4%; Pred. No. 7.1;
Matches 13; Conservative 3; Mismatches 10; Indels 2; Gaps 2;

QY 1 CRXNOKCFQHLDDCCSRKCNRFN-KCV 27
   | : : : : | | | | |
Db 28 CARNNEYCLTH-RDCSGSGCLSPSKCV 54

RESULT 15
Q9U4A2 PRELIMINARY; PRT; 1685 AA.
AC Q9U4A2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 26, Last annotation update)
DE Variant surface protein PfEMP1 (fragment).
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```
GN Name=var;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20144115; PubMed=10677532; DOI=10.1073/pnas.040545897;
RA Smith J.D., Graig A.G., Kriek N., Hudson-Taylor D., Kyes S., Fagen T.,
RA Pinches R., Baruch D.I., Newbold C.I., Miller L.H.;
RT Identification of a Plasmodium falciparum intercellular adhesion
RT molecule-1 binding domain: a parasite adhesion trait implicated in
RT cerebral malaria.
RL Proc. Natl. Acad. Sci. U.S.A. 97:1766-1771 (2000).
DR EMBL; AF193424; AAF1980.1; -.
DR GO; GO:0005539; F:glycosaminoglycan binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR000454; Eub ATPase_Caub.
DR InterPro; IPR004258; PFEMP.
DR Pfam; PF03011; PFEMP; 1.
DR PROSITE; PS00605; ATPase_C; UNKNOWN_1.
FT NON_TER 1685 1685
SQ SEQUENCE 1685 AA; 193671 MW; D1FD426666B0551E CRC64;

Query Match      37.3%; Score 60; DB 2; Length 1685;
Best Local Similarity 33.3%; Pred. No. 60;
Matches 9; Conservative 7; Mismatches 9; Indels 2; Gaps 1;

QY 1 CRXNOKCFQHLDDCCSRKCNRFNK 25
   | : : : : | | | | |
Db 1048 CKTKKKCTNKSDDCNTCTEACTAYNR 1074

RESULT 16
Q7PM27 PRELIMINARY; PRT; 638 AA.
AC Q7PM27;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000014402 (Fragment).
GN Name=ENSANGG0000011913;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100898; EAA14483.2; -.
DR HSSP; PI9438; IEXT.
DR InterPro; IPR003341; DUF139.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF02363; C tripleX; 15.
DR Pfam; PF00008; EGF; 1.
DR PROSITE; PS01186; EGF_2; 4.
FT NON_TER 638 638
SQ SEQUENCE 638 AA; 69390 MW; 026DB44846AB483F CRC64;

Query Match      36.6%; Score 59; DB 2; Length 638;
Best Local Similarity 36.0%; Pred. No. 34;
Matches 9; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 RIXNOKCFQHLDDCCSRKCNRFNK 26
   | : : : : | | | | |
Db 30 RLSNHRCLPHCDDCDNGICTKPGYC 54
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DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR001841; Znf_ring.
 DR Pfam: PF00008; EGF; 5.
 DR PRINTS: PR00010; EGFBL00D.
 DR SMART: SM00181; EGF; 6.
 DR SMART: SM00179; EGF CA; 4.
 DR PROSITE: PS00010; ASX HYDROXYL; 2.
 DR PROSITE: PS00022; EGF 1; 6.
 DR PROSITE: PS01186; EGF 2; 6.
 DR PROSITE: PS00026; EGF 3; 6.
 DR PROSITE: PS01187; EGF CA; 2.
 KW Alternative splicing; Calcium; Calcium-binding; EGF-like domain;
 Repeat; Signal; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 383
 FT DOMAIN 27 306
 FT TRANSMEM 307 327
 FT DOMAIN 328 383
 FT DOMAIN 27 58
 FT DOMAIN 62 89
 FT DOMAIN 91 129
 FT DOMAIN 131 172
 FT DOMAIN 174 210
 FT DOMAIN 212 248
 FT DISULFID 29 40
 FT DISULFID 33 46
 FT DISULFID 48 57
 FT DISULFID 66 71
 FT DISULFID 79 88
 FT DISULFID 95 107
 FT DISULFID 101 117
 FT DISULFID 119 128
 FT DISULFID 135 148
 FT DISULFID 142 160
 FT DISULFID 162 171
 FT DISULFID 178 189
 FT DISULFID 183 198
 FT DISULFID 200 209
 FT DISULFID 216 227
 FT DISULFID 221 236
 FT DISULFID 238 247
 FT CARBOHYD 157 157
 FT VARSPIC 1 179
 SQ SEQUENCE 383 AA; 40547 MW; 701AC68043863EA7 CRC64;
 Query Match 36.0%; Score 58; DB 1; Length 383;
 Best Local Similarity 52.6%; Pred. No. 28;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 8 CFOHLDCCSRKCNRNKC 26
 Db 209 CTINLDDCASRPCQRCARGC 227
 RESULT 20
 SCX1 OPICA
 ID SCX1 OPICA STANDARD; PRT; 66 AA.
 AC P60252;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Opicalcine 1 precursor.
 OS Opisthophthalmus carinatus (African yellow leg scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Tardigrada; Scorpionoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
 OX NCBI_TaxID=190115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
 RA Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
 RT "Evolutionary origin of inhibitor cysteine knot peptides.";
 FASEB J. 17:1765-1767(2003).
 CC -!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the scorpion calcine family.
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 DR EMBL: AY225784; AAP73822.1;
 KW Calcium channel inhibitor; Neurotoxin; Signal; Toxin.
 FT SIGNAL 1 22
 FT PROPEP 23 33
 FT CHAIN 34 66
 FT DISULFID 36 50
 FT DISULFID 43 54
 FT DISULFID 49 65
 FT SEQUENCE 66 AA; 7644 MW; 2CC779B9F3AEF41 CRC64;
 Query Match 35.4%; Score 57; DB 1; Length 66;
 Best Local Similarity 47.6%; Pred. No. 8;
 Matches 10; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
 QY 8 CQHL-----DDCSRKCNR 22
 Db 36 CLPHLRCKENNDCCSKCKR 56
 RESULT 21
 SCX2 OPICA
 ID SCX2 OPICA STANDARD; PRT; 66 AA.
 AC P60253;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Opicalcine 2 precursor.
 OS Opisthophthalmus carinatus (African yellow leg scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Tardigrada; Scorpionoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
 OX NCBI_TaxID=190115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
 RA Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
 RT "Evolutionary origin of inhibitor cysteine knot peptides.";
 FASEB J. 17:1765-1767(2003).
 CC -!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the scorpion calcine family.
 KW Calcium channel inhibitor; Neurotoxin; Signal; Toxin.
 FT SIGNAL 1 22
 FT PROPEP 23 33
 FT CHAIN 34 66
 FT DISULFID 36 50
 FT DISULFID 43 54
 FT DISULFID 49 65
 FT SEQUENCE 66 AA; 7644 MW; 6DC7632E9F205F5D CRC64;

RL FASEB J. 17:1765-1767(2003).
 CC -!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the scorpion calcine family.
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 DR EMBL: AY225784; AAP73822.1;
 KW Calcium channel inhibitor; Neurotoxin; Signal; Toxin.
 FT SIGNAL 1 22
 FT PROPEP 23 33
 FT CHAIN 34 66
 FT DISULFID 36 50
 FT DISULFID 43 54
 FT DISULFID 49 65
 FT SEQUENCE 66 AA; 7644 MW; 2CC779B9F3AEF41 CRC64;
 Query Match 35.4%; Score 57; DB 1; Length 66;
 Best Local Similarity 47.6%; Pred. No. 8;
 Matches 10; Conservative 2; Mismatches 3; Indels 6; Gaps 1;
 QY 8 CQHL-----DDCSRKCNR 22
 Db 36 CLPHLRCKENNDCCSKCKR 56

RESULT 21
 SCX2 OPICA
 ID SCX2 OPICA STANDARD; PRT; 66 AA.
 AC P60253;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Opicalcine 2 precursor.
 OS Opisthophthalmus carinatus (African yellow leg scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Tardigrada; Scorpionoidea; Scorpionidae; Scorpioninae; Opisthophthalmus.
 OX NCBI_TaxID=190115;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=22838230; PubMed=12958203; DOI=10.1096/fj.02-1044fje;
 RA Zhu S.-Y., Darbon H., Dyason K., Verdonck F., Tytgat J.;
 RT "Evolutionary origin of inhibitor cysteine knot peptides.";
 FASEB J. 17:1765-1767(2003).
 CC -!- FUNCTION: Potently and reversibly modifies channel gating behavior of the type 1 ryanodine receptor (RyR1) by inducing prominent subconductance behavior. Binds a different site as ryanodine (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- SIMILARITY: Belongs to the scorpion calcine family.
 KW Calcium channel inhibitor; Neurotoxin; Signal; Toxin.
 FT SIGNAL 1 22
 FT PROPEP 23 33
 FT CHAIN 34 66
 FT DISULFID 36 50
 FT DISULFID 43 54
 FT DISULFID 49 65
 FT SEQUENCE 66 AA; 7644 MW; 6DC7632E9F205F5D CRC64;

```

Query Match          35.4%; Score 57; DB 1; Length 66;
Best Local Similarity 47.6%; Pred. No. 8;
Matches 10; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

Qy      8 CFQHL-----DDCSRKCNR 22
      |||
      36 CLPHLKRCCKENNDCCSRKCKR 56
      |||

RESULT 22
Q7Q0M5      PRELIMINARY;      PRT;      650 AA.
ID Q7Q0M5
AC Q7Q0M5
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eb1p2886 (Fragment)
GN Name=ebiG2886; ORFNames=ENSANGG0000002379;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data. EAAL4361.1; -.
DR EMBL; AAB01008980; EAAL4361.1; -.
DR HSSP; P00740; LEDM.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0007154; P:cell communication; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR001774; DSL.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF01414; DSL; 1.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF07645; EGF_Ca; 1.
DR PRINTS; PR00010; EGFBL00D.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS00026; EGF_3; 7.
DR PROSITE; PS01187; EGF_CA; 2.
DR EGF-like domain.
FT NON_TER 1
FT NON_TER 650
SQ SEQUENCE 650 AA; 71172 MW; 19C43512C5B8FCC8 CRC64;

Query Match          35.4%; Score 57; DB 2; Length 650;
Best Local Similarity 33.3%; Pred. No. 60;
Matches 8; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy      4 XNQCFOHLLDDCSRKCNRFNKC 27
      |||
      15 QNEKSIDHNEKCCSEKADAQGRCI 38
      |||

RESULT 23
O42374      PRELIMINARY;      PRT;      752 AA.
ID O42374
AC O42374
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Notch receptor protein (Fragment).
GN Name=notch2; Synonyms=Notch6;

```

DR GO; GO:0005524; F-ATP binding; IEA.
 DR GO; GO:0042626; F-ATPase activity, coupled to transmembrane m. . .; IEA.
 DR GO; GO:0007059; P:chromosome segregation; IEA.
 DR GO; GO:0008610; P:transport; IEA.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR003405; SMC C.
 DR InterPro; IPR010935; SMC hinge.
 DR InterPro; IPR003395; SMC N.
 DR Pfam; PF02483; SMC C; 1.
 DR Pfam; PF06470; SMC hinge; 1.
 DR Pfam; PF02463; SMC N; 1.
 SQ SEQUENCE 1245 AA; 142930 MW; C93C54289FEA2500 CRC64;
 Query Match 35.4%; Score 57; DB 2; Length 1245;
 Best Local Similarity 42.9%; Pred. No. 1.le-02;
 Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 6 KQCFQHLDDCCSKCNKFNKC 26
 DB 1056 KRCQEFQVKFQRCQFNKC 1076
 RESULT 25
 NCOTC_XENLA STANDARD; PRT; 2524 AA.
 ID NCOTC_XENLA STANDARD; PRT; 2524 AA.
 AC P21783;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurogenic locus notch protein homolog precursor (XOTCH protein).
 GN Name=XOTCH;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90385285; PubMed=2402639;
 RA Coffman C., Harris W., Kintner C.;
 RT "Xotch, the Xenopus homolog of Drosophila notch."; Science 249:1438-1441(1990).
 RL [2]
 RP REVISIONS TO 1759-1782.
 RA Kintner C.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DEVELOPMENTAL STAGE: Expressed almost uniformly in early embryos.
 CC -!- SIMILARITY: Belongs to the NOTCH family.
 CC -!- SIMILARITY: Contains 6 ANK repeats.
 CC -!- SIMILARITY: Contains 36 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -----
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 CC -----
 CC EMBL; M33874; AAB02039.1; --
 DR HSSP; P46531; 1PB5
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.

DR Pfam; PF00008; EGF; 36.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSE; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF CA; 24.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS02027; ANK_REPEAT; 1.
 DR PROSITE; PS00088; ANK_REPEAT; 4.
 DR PROSITE; PS00010; ASX_HYDROXYL; 23.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 29.
 DR PROSITE; PS00026; EGF_3; 36.
 DR PROSITE; PS01187; EGF CA; 21.
 KW ANK repeat; Differentiation; EGF-like domain; Glycoprotein;
 KW Neurogenesis; Notch signaling; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 19
 FT CHAIN 20 2524
 FT DOMAIN 20 1728
 FT TRANSMEM 1729 1750
 FT DOMAIN 1751 2524
 FT DOMAIN 20 57
 FT DOMAIN 58 99
 FT DOMAIN 102 140
 FT DOMAIN 141 177
 FT DOMAIN 179 215
 FT DOMAIN 217 254
 FT DOMAIN 256 292
 FT DOMAIN 294 332
 FT DOMAIN 334 370
 FT DOMAIN 371 409
 FT DOMAIN 411 449
 FT DOMAIN 451 487
 FT DOMAIN 489 525
 FT DOMAIN 527 563
 FT DOMAIN 565 600
 FT DOMAIN 602 638
 FT DOMAIN 640 675
 FT DOMAIN 677 713
 FT DOMAIN 715 750
 FT DOMAIN 752 788
 FT DOMAIN 790 826
 FT DOMAIN 828 866
 FT DOMAIN 868 904
 FT DOMAIN 906 942
 FT DOMAIN 944 980
 FT DOMAIN 982 1018
 FT DOMAIN 1020 1056
 FT DOMAIN 1058 1094
 FT DOMAIN 1096 1142
 FT DOMAIN 1144 1180
 FT DOMAIN 1182 1218
 FT DOMAIN 1220 1264
 FT DOMAIN 1266 1304
 FT DOMAIN 1306 1346
 FT DOMAIN 1347 1383
 FT DOMAIN 1386 1424
 FT REPEAT 1441 1478
 FT REPEAT 1479 1520
 FT REPEAT 1521 1560
 FT REPEAT 1560 1594
 FT REPEAT 1594 1628
 FT REPEAT 1628 1662
 FT REPEAT 1662 1696
 FT REPEAT 1696 1730
 FT REPEAT 1730 1764
 FT REPEAT 1764 1798
 FT REPEAT 1798 1832
 FT REPEAT 1832 1866
 FT REPEAT 1866 1900
 FT REPEAT 1900 1934
 FT REPEAT 1934 1968
 FT REPEAT 1968 2002
 FT REPEAT 2002 2036
 FT REPEAT 2036 2070
 FT DISULFID 22 35
 FT DISULFID 29 45
 FT DISULFID 47 56
 FT DISULFID 62 74

FT	DISULFID	1046	1055	By similarity.
FT	DISULFID	1062	1073	By similarity.
FT	DISULFID	1067	1082	By similarity.
FT	DISULFID	1084	1093	By similarity.
FT	DISULFID	1100	1121	By similarity.
Query Match 35.4%; Score 57; DB 1; Length 2524;				
Best Local Similarity 37.5%; Pred. No. 2e+02;				
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;				
Qy	4 XNOKCFQHLDDCCSRKCNRENKCV 27			
Db	249 SGQNCENIIDCPSNCRNGGTCV 272			
RESULT 26				
Q891K4	PRELIMINARY; PRT; 153 AA.			
ID	Q891K4			
AC	Q891K4;			
DT	01-JUN-2003 (TReMBLrel. 24, Created)			
DT	01-JUN-2003 (TReMBLrel. 24, Last sequence update)			
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)			
DE	Membrane-associated protein.			
GN	OrderedLocusNames=CTC02367;			
OS	Clostridium tetani.			
OC	Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_TaxID=1513;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Massachusetts / E88;			
RX	MEDLINE=2457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;			
RA	Brueggemann H., Baesumer S., Fricke W.F., Wierer A., Liesegang H.,			
RA	Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,			
RA	Gottschalk G.;			
RT	"The genome sequence of Clostridium tetani, the causative agent of			
RT	tetanus disease."			
RL	Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).			
DR	EMBL; AE015944; AA036841.1; -.			
KW	Complete proteome.			
SQ	SEQUENCE 153 AA; 17382 MW; 6334C88F39A8E189 CRC64;			
Query Match 35.1%; Score 56.5; DB 2; Length 153;				
Best Local Similarity 38.5%; Pred. No. 19;				
Matches 10; Conservative 3; Mismatches 10; Indels 3; Gaps 1;				
Qy	1 CRXNOKCFQHLDDCCSRK---CNRP 23			
Db	114 CSGKDDKCHHHHDNCCHHHGGCENN 139			
RESULT 27				
Q24821	PRELIMINARY; PRT; 194 AA.			
ID	Q24821			
AC	Q24821;			
DT	01-NOV-1996 (TReMBLrel. 01, Created)			
DT	01-NOV-1996 (TReMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TReMBLrel. 26, Last annotation update)			
DE	GalNA lectin heavy subunit (Fragment).			
GN	Name=hgl4.			
OS	Entamoeba histolytica.			
OC	Eukaryota; Entamoebidae; Entamoeba.			
OX	NCBI_TaxID=5759;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=HMI:IMSS;			
RA	Ramakrishnan G., Ragland B.D., Purdy J.E., Mann B.J.;			
RL	Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U33443; AAA75551.1; -.			
DR	PIR; S70663; S70663.			
DR	GO; GO:0005529; F:sugar binding; IEA.			
DR	InterPro; IPR06209; EGF like.			
DR	PROSITE; PS00022; EGF 1; UNKNOWN 1.			

KW Lectin.
 FT NON TER 1 1
 FT NON TER 194 194
 SQ SEQUENCE 194 AA; 21501 MW; BDQC3HD9406AA858 CRC64;
 Query Match 35.1%; Score 56.5; DB 2; Length 194;
 Best Local Similarity 43.3%; Pred. No. 24;
 Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKKCFQHLDDCCSRK--CNRFN-KCV 27
 DB 119 CSMGTDNIITYHDDCNSRKSQCNGFNKCV 148
 NCBI_TaxID=5759;

RESULT 28
 Q8MU89 PRELIMINARY; PRT; 372 AA.
 ID Q8MU89
 AC Q8MU89
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gal/GalNAc lectin heavy subunit region D (Fragment).
 GN Name=hgl;
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
 RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
 RA Pearson W.R., Loftus B., Petri W.A. Jr.;
 RT "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
 from clinical isolates."
 RL Exp. Parasitol. 101:157-163(2002).
 DR EMBL; AF533541; AAM97358.1; -;
 DR GO; GO:0005529; F:sugar binding; IEA.
 KW Lectin.
 FT NON TER 1 1
 FT NON TER 372 372
 SQ SEQUENCE 372 AA; 41984 MW; 5BE2A013D596D124 CRC64;
 Query Match 35.1%; Score 56.5; DB 2; Length 372;
 Best Local Similarity 43.3%; Pred. No. 42;
 Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKKCFQHLDDCCSRK--CNRFN-KCV 27
 DB 80 CSMGTDNIITYHDDCNSRKSQCNGFNKCV 109
 NCBI_TaxID=5759;

RESULT 29
 Q8MZT3 PRELIMINARY; PRT; 372 AA.
 ID Q8MZT3
 AC Q8MZT3
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gal/GalNAc lectin heavy subunit region D (Fragment).
 GN Name=hgl;
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
 RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
 RA Pearson W.R., Loftus B., Petri W.A. Jr.;
 RT "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
 from clinical isolates."
 RL Exp. Parasitol. 101:157-163(2002).
 DR EMBL; AF501276; AAM2197.1; -;
 DR GO; GO:0005529; F:sugar binding; IEA.
 KW Lectin.
 FT NON TER 1 1
 FT NON TER 372 372
 SQ SEQUENCE 372 AA; 41984 MW; 5BE2A013D596D124 CRC64;
 Query Match 35.1%; Score 56.5; DB 2; Length 372;
 Best Local Similarity 43.3%; Pred. No. 42;
 Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKKCFQHLDDCCSRK--CNRFN-KCV 27
 DB 80 CSMGTDNIITYHDDCNSRKSQCNGFNKCV 109
 NCBI_TaxID=5759;

RESULT 30
 Q24835 PRELIMINARY; PRT; 1292 AA.
 ID Q24835
 AC Q24835
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Galactose-specific adhesin 170kD subunit precursor.
 GN Name=hgl3;
 OS Entamoeba histolytica.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OX NCBI_TaxID=5759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91195330; PubMed=2014248;
 RA Mann B.J., Torian B.E., Vedvick T.S., Petri W.A. Jr.;
 RT "Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
 histolytica."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3248-3252(1991).
 DR EMBL; AF533541; AAM97358.1; -;
 DR GO; GO:0005529; F:sugar binding; IEA.
 KW Lectin.
 FT NON TER 1 1
 FT NON TER 372 372
 SQ SEQUENCE 372 AA; 41984 MW; 5BE2A013D596D124 CRC64;
 Query Match 35.1%; Score 56.5; DB 2; Length 372;
 Best Local Similarity 43.3%; Pred. No. 42;
 Matches 13; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKKCFQHLDDCCSRK--CNRFN-KCV 27
 DB 80 CSMGTDNIITYHDDCNSRKSQCNGFNKCV 109
 NCBI_TaxID=5759;

RESULT 31
 Q8I218 PRELIMINARY; PRT; 3467 AA.
 ID Q8I218
 AC Q8I218
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Erythrocyte membrane protein 1 (PFEMP1).
 GN Name=VAR; Synonyms=PF00202C;
 RN [1]

OS Plasmodium_falciparum (isolate 3D7).
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=36329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2255708; PubMed=12368867; DOI=10.1038/nature01095;
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
 RA Feltwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
 RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,
 RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitz E.,
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
 RA Seger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13."
 RL Nature 419:527-531(2002).
 DR EMBL: AL034557; CAD49096.1;
 DR GO: GO:0005339; F:glycosaminoglycan binding; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR000345; CytC_heme_BS.
 DR Pfam: PF03011; PFEMP.2.
 DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN 1.
 SQ SEQUENCE 3467 AA; 398216 MW; E8FCBA37025989D2 CRC64;
 Query Match 35.1%; Score 56.5; DB 2; Length 3467;
 Best Local Similarity 31.9%; Pred. No. 3e+02;
 Matches 15; Conservative 3; Mismatches 8; Indels 21; Gaps 2;
 OY 1 CRXNQK-----CFQHLDDCCSR-----KCNRFNKC 26
 DB 318 CRIRNHKLKIKDACRNDKRLYCSQNGYDCTKRIEKGSSCSRNC 364
 RESULT 32
 ID Q9IAT6 PRELIMINARY; PRT; 664 AA.
 AC Q9IAT6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DeltaC.
 GN Name:deltaC; Synonyms:deltaC; (Danio rerio).
 OS Brachydanio rerio (zebrafish)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20054100; PubMed=10585570; DOI=10.1016/S0925-4773(99)00231-2;
 RA Smithers L.E., Haddon C., Jiang Y.-J., Lewis J.;
 RT "Sequence and embryonic expression of deltaC in the zebrafish."
 RL Mech. Dev. 90:119-123(2000).
 DR EMBL: AF146429; AAF27299.1;
 DR HSSP: P00740; LEDM.
 DR ZFIN: ZDB-GENE-000125-4; dlc.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0007154; P:cell communication; IEA.
 DR InterPro: IPR000152; Aex_hydroxyl_S.
 DR InterPro: IPR001774; DSL.
 DR InterPro: IPR000742; EGF 2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR006209; EGF_like.

DR Pfam: PF01414; DSL; 1.
 DR Pfam: PF00008; EGF; 7.
 DR PRINTS: PR00010; EGFBL00D.
 DR SMART: SM00051; DSL; 1.
 DR SMART: SM00179; EGF_CA; 4.
 DR PROSITE: PS00010; ASX_HYDROXYL; 2.
 DR PROSITE: PS00022; EGF_1; 8.
 DR PROSITE: PS01186; EGF_2; 8.
 DR PROSITE: PS00026; EGF_3; 6.
 DR PROSITE: PS01187; EGF_CA; 2.
 KW EGF-like domain.
 SQ SEQUENCE 664 AA; 72547 MW; 0AD6C34C8579116B CRC64;
 Query Match 34.8%; Score 56; DB 2; Length 664;
 Best Local Similarity 34.5%; Pred. No. 81;
 Matches 10; Conservative 4; Mismatches 13; Indels 2; Gaps 1;
 OY 1 CR--IXNQKCFQHLDDCCSRKCNRFNKC 27
 DB 408 CRFGFTGSRCEITNIDDCSSNPNQAGTCV 436
 RESULT 33
 ID Q9LGM8 PRELIMINARY; PRT; 708 AA.
 AC Q9LGM8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Similar to Arabidopsis thaliana chromosome V P1 MJJ3 (Similar to
 DE Arabidopsis thaliana chromosome V P1 MJJ3; MJJ3.6).
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu J., Niumura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijishita S., Honda M., Ichikawa Y., Idenuma A., Iijima M., Ikeda M.,
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF002521; BAA96756.2;
 DR EMBL: AF002539; BAA08195.2;
 DR Gramene; Q9LGM8;
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:000151; C:ubiquitin ligase complex; IEA.
 DR GO: GO:0003700; F:transcription factor activity; IEA.
 DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR GO: GO:0016567; P:protein ubiquitination; IEA.
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro: IPR006058; 2Fe2S fd BS.
 DR InterPro: IPR000967; Znf_NFX1.
 DR InterPro: IPR001965; Znf_PHD.
 DR InterPro: IPR001841; Znf_ring.

"Deltex acts as a positive regulator of Notch signaling through the *Notch1* receptor." *Development* 130:117-127.

interactions' with the Notch ankyrin repeats."; Development 121:2633-2644 (1995).
[10]
S3 CLEAVAGE BY PSN.
RX MEDLINE=99221487; PubMed=10206646; DOI=10.1038/19091;
RA Struhl G., Greenwald I.,
RT "Presenilin is required for activity and nuclear access of Notch in Drosophila."; Nature 398:522-525 (1999).
[11]
S3 CLEAVAGE BY PSN.
RX MEDLINE=99221488; PubMed=10206647; DOI=10.1038/19096;
RA Ye Y., Lukinova N., Fortini M.E.;
RT "Neurogenic phenotypes and altered Notch processing in Drosophila Presenilin mutants."; Nature 398:525-529 (1999).
[12]
S2 CLEAVAGE BY KUZ.
RX MEDLINE=21657146; PubMed=11799064; DOI=10.1101/gad.942302;
RA Lieber T., Kidd S., Young M.W.;
RT "kuzbanian-mediated cleavage of Drosophila Notch."; Genes Dev. 16:209-221 (2002).
[13]
MUTANT MCD5.
RX MEDLINE=21575956; PubMed=11719214; DOI=10.1016/S0960-9822(01)00562-0;
RA Ramain P., Khechumian K., Seugnet L., Arbogast N., Ackermann C., Heitzler P.;
RT "Novel Notch alleles reveal a Deltex-dependent pathway repressing neural fate."; Curr. Biol. 11:1729-1738 (2001).
[14]
RX MEDLINE=22256570; PubMed=12369105;
RA Portin P.;
RT "General outlines of the molecular genetics of the Notch signalling pathway in Drosophila melanogaster: a review."; Hereditas 136:89-96 (2002).
CC -!- FUNCTION: Signaling protein, which regulates, with both positive and negative signals, the differentiation of at least central and peripheral nervous system and eye, wing disk, oogenesis, segmental appendages such as antennae and legs, and muscles, through lateral inhibition or induction. Functions as a receptor for membrane-bound ligands Delta and Serrate to regulate cell-fate determination. Upon ligand activation, and releasing from the cell membrane, the Notch intracellular domain (NICD) forms a transcriptional activator complex with Su(H) (Suppressor of hairless) and activates genes of the E(spl) complex. Essential for proper differentiation of ectoderm.
CC -!- SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx via its ANK repeats.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and S3 cleavage, it is released from the cell membrane and enters into the nucleus in conjunction with Su(H).
CC -!- PTM: Upon binding its ligands such as Delta or Serrate, it is cleaved (S2 cleavage) in its extracellular domain, close to the transmembrane domain. S2 cleavage is probably mediated by Kuz. It is then cleaved (S3 cleavage) downstream of its transmembrane domain, releasing it from the cell membrane. S3 cleavage requires Pen.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 6 ANK repeats.
CC -!- SIMILARITY: Contains 36 EGF-like domains.
CC -!- SIMILARITY: Contains 13 Notch repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Query Match 34.8%; Score 56; DB 1; Length 2703;
Best Local Similarity 33.3%; Pred. No. 2.8e+02;
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
QY 4 XNOKCFQHLDDCCSRKCNRFNKC 27
DB 822 TGQCTNIDDDCVNFCNGGTCT 845
RESULT 35
CXOB CONMA STANDARD; PRT; 25 AA.
AC P05485;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin MVIIB (SNX-159).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE.
RX MEDLINE=87299637; PubMed=2441741;
RA Olivera B.M., Cruz L.J., de Santos V., Lechmanant G.W., Griffin D., Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R., Rivier J.E.;
RT "Neuronal calcium channel antagonists. Discrimination between calcium channel subtypes using omega-conotoxin from Conus magus venom."; Biochemistry 26:2086-2090 (1987).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind and block voltage-sensitive calcium channels (VSCC).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type family.
CC PIR; JH0701; JH0701.
DR HSSP; P05484; 1DM4.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT DISULFID 1 16
FT DISULFID 8 20
FT DISULFID 15 25
FT MOD RES 25 25 Cysteine amide.
SQ SEQUENCE 25 AA; 2626 MW; E4B9CE5EPAA3734D CRC64;
Query Match 34.5%; Score 55.5; DB 1; Length 25;
Best Local Similarity 38.5%; Pred. No. 5.2;
Matches 10; Conservative 4; Mismatches 11; Indels 1; Gaps 1;
QY 1 CRXNOKCFQHLDDCCSRKCNRFNKC 26
DB 1 CKGKGASCHRTSYDCTGSCNR-GKC 25
RESULT 36
Q24822 PRELIMINARY; PRT; 194 AA.
AC Q24822;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE GalNAC lectin heavy subunit (Fragment).
GN Name-hgl5;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM1:IMS;
RA Ramakrishnan G., Ragland B.D., Purdy J.E., Mann B.J.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

```
DR EMBL; U33444; AAA75552.1; -
DR PIR; S70664; S70664.
DR GO; GO:0005529; F:sugar binding; IEA.
DR InterPro; IPR006209; EGF-like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
FT NON TER 1 1
FT NON TER 194 194
SQ SEQUENCE 194 AA; 21438 MW; 8A9DFEFC481C671D CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 194;
Best Local Similarity 40.0%; Pred. No. 32;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
Db 119 CSMGTDNVIYHDDCNSRKSCQGNFGKCI 148

RESULT 37
QBMZT1 ID QBMZT1 PRELIMINARY; PRT; 372 AA.
AC QBMZT1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gal/GalNAc lectin heavy subunit region D (Fragment).
GN Name=hgl;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
RA Pearson W.R., Loftus B., Petri W.A. Jr.;
RT "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501278; AAM22199.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41994 MW; 49AA800C6ECE259F CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
Db 80 CSMGTDNVIYHDDCNSRKSCQGNFGKCI 109

RESULT 38
QBMZT2 ID QBMZT2 PRELIMINARY; PRT; 372 AA.
AC QBMZT2;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gal/GalNAc lectin heavy subunit region D (Fragment).
GN Name=hgl;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22314996; PubMed=12427470; DOI=10.1016/S0014-4894(02)00113-3;
RA Beck D.L., Tanyuksel M., Mackey A.J., Haque R., Traipaidze N.,
RA Pearson W.R., Loftus B., Petri W.A. Jr.;
RT "Entamoeba histolytica: sequence conservation of the Gal/GalNAc lectin
from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501278; AAM22199.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41994 MW; 49AA800C6ECE259F CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
Db 80 CSMGTDNVIYHDDCNSRKSCQGNFGKCI 109

from clinical isolates.";
RL Exp. Parasitol. 101:157-163(2002).
DR EMBL; AF501277; AAM22198.1; -
DR GO; GO:0005529; F:sugar binding; IEA.
KW Lectin.
FT NON TER 1 1
FT NON TER 372 372
SQ SEQUENCE 372 AA; 41961 MW; 1FF00CE222BFF5100 CRC64;

Query Match 34.5%; Score 55.5; DB 2; Length 372;
Best Local Similarity 40.0%; Pred. No. 56;
Matches 12; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
   : : : : : : : : : : : : : : : :
Db 80 CSMGTDNVIYHDDCNSRKSCQGNFGKCI 109

RESULT 39
GILI_ENTHI ID GILI_ENTHI STANDARD; PRT; 1276 AA.
AC F32022;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Galactose-inhibitable lectin 170 kDa subunit.
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=91195330; PubMed=2014248;
RA Mann B.J., Torian B.E., Vedvick T.S., Petri W.A. Jr.;
RT "Sequence of a cysteine-rich galactose-specific lectin of Entamoeba
histolytica.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3248-3251(1991).
CC -!- FUNCTION: Lectin that binds galactose.
CC -!- SURUNIT: Heterodimer of a heavy (170 kDa) and a light subunit (35
kDa) linked by disulfide bonds.
CC -!- PTM: N-glycosylated.
CC
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
DR EMBL; M59850; -; NOT ANNOTATED CDS.
KW Direct protein sequencing; Glycoprotein; Lectin; Transmembrane.
FT TRANSMEM 1210 1235 Potential.
FT CARBOHYD 79 79 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 218 218 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 245 245 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 361 361 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 374 374 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 452 452 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 471 471 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 627 627 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 643 643 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 874 874 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 976 976 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1122 1122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1187 1187 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1197 1197 N-linked (GlcNAc...) (Potential).
FT VARIANT 441 441 R -> K.
SQ SEQUENCE 1276 AA; 143239 MW; A6B903F11DC2D5B4 CRC64;

Query Match 34.5%; Score 55.5; DB 1; Length 1276;
Best Local Similarity 40.0%; Pred. No. 1.7e+02;
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Matches 12;., Conservative 4; Mismatches 11; Indels 3; Gaps 2;
QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KCV 27
D5 702 CSMGTDNIITYHDDCSKSCQCGNFKCI 731

RESULT 40
ID SCXC SCOMA STANDARD; PRT; 33 AA.
AC P60254;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Maurocalcine (MCA).
OS Scorpio maurus palnatus (Chactoid scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Turlida; Scorpionoidea; Scorpionidae; Scorpioninae; Scorpio.
OX NCBI_TaxID=53957;
RN [1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP PubMed=10713267; DOI=10.1016/S0014-5793(00)01239-4;
RA Fajloun Z., Kharrat R., Chen L., Lecomte C., Di Luccio E., Bichet D.,
RA El Ayeub M., Rochat H., Allen P.D., Pessah I.N., De Waard M.,
RA Sabatier J.M.;
RT "A new fold in the scorpion toxin family, associated with an activity
on a ryanodine-sensitive calcium channel.";
RL Proteins 40:436-442(2000).
RP STRUCTURE BY NMR.
RX MEDLINE=200211140; PubMed=10861934;
RX DOI=10.1002/1097-0134(20000815)40:3<436::AID-PROT90>3.0.CO;2-9;
RA Mosbah A., Kharrat R., Fajloun Z., Renisio J.-G., Blanc E.,
RA Sabatier J.-M., El Ayeub M., Darbon H.;
RT "A new fold in the scorpion toxin family, associated with an activity
on a ryanodine-sensitive calcium channel.";
RL Proteins 40:436-442(2000).
CC -1- FUNCTION: Potently and reversibly modifies channel gating behavior
of the type 1 ryanodine receptor (RyR1) by inducing prominent
subconductance behavior. Binds a different site as ryanodine.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=3858.2; METHOD=WALDI; RANGE=1-33;
NOTE=Ref.1.
CC -1- TOXIC DOSE: LD(50) is 20 ug/mice by intracerebroventricular
injection.
CC -1- SIMILARITY: Belongs to the scorpion calcine family.
DR FDB; IC50; NMR; -.
KW 3D-structure; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Toxin.
FT DISULFID 3 17
FT DISULFID 10 21
FT DISULFID 16 32
SQ SEQUENCE 33 AA; 3855 MW; ASFE70F945FEC8E6 CRC64;

Query Match 34.2%; Score 55; DB 1; Length 33;
Best Local Similarity 47.6%; Pred. No. 7.6;
Matches 10; Conservative 1; Mismatches 4; Indels 6; Gaps 1;
QY 8 CFQHL-----DDCCSRKCNR 22
D5 3 CLPHLKCKENKDCCKKCR 23

RESULT 41
Q9PSU2 PRELIMINARY; PRT; 112 AA.
AC Q9PSU2;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Homeobox protein Lim-1 (fragment).
GN Name=Xlim-1;

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OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97420748; PubMed=9275190; DOI=10.1073/pnas.94.18.9717;
RA Rebert M.L., Dawid I.B.;
RT "Transcriptional regulation of the Xlim-1 gene by activin is mediated
by an element in intron 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:9717-9722(1997)
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
DR EMBL; AF013242; AAB70190.1; -.
DR HSSP; P70662; 1M3V.
DR GO; GO:0005634; C:nucleus; IEA.
DR InterPro; IPR001781; LIM.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00478; LIM DOMAIN 1; 2.
DR PROSITE; PS00023; LIM DOMAIN 2; 2.
KW LIM domain; Metal-binding; Nuclear protein; Zinc.
FT NON TER 112 112
SQ SEQUENCE 112 AA; 12975 MW; F491D6CCF80D882F CRC64;

Query Match 34.2%; Score 55; DB 2; Length 112;
Best Local Similarity 44.0%; Pred. No. 22;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;
QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
D5 22 RAHWKVCVQ----CCECKCNLTCK 42

RESULT 42
Q7XKS9 PRELIMINARY; PRT; 380 AA.
AC Q7XKS9;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE OSJNBa003821.2 protein.
GN Name=OSJNBa003821.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X.,
RA Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L.,
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,
RA Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL731588; CAE05509.1; -.
DR HSSP; O49397; 1IRZ.
DR Gramene; O7XKS9; -.
DR GO; GO:003677; F:DNA binding; IEA.
DR GO; GO:000156; F:two-component response regulator activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:000160; P:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR011006; CheY like.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR006447; Myb_SHAQKYP.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.

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DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00448; REC; 1.
DR TIGRFAMS; TIGR01557; myb_SHAOKYP; 1.
DR PROSITE; PS00110; RESPONSE_REGULATORY; 1.
DR PHOSPHORYLATION; Sensory transduction.
KW Phosphorylation; Sensory transduction.
SQ SEQUENCE 380 AA; 42765 MW; 69DBD43F0CD200E1 CRC64;

Query Match      34.2%; Score 55; DB 2; Length 380;
Best Local Similarity 44.0%; Pred. No. 65;
Matches 11; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 3 IXNQKCFQHLDDCCSRKCNRFNKC 27
DB 17 IDEDKC--HADSTCSMICTQLNFCV 39

RESULT 43
LHX5_XENLA
ID LHX5_XENLA STANDARD; PRT; 402 AA.
AC P37137;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx5 (Homeobox protein LIM-5) (XLIM-5) (XLIM-2A).
GN Name=LHX5; Synonyms=LIM-2A, LIM2A, LIM5;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95377545; PubMed=7649385; DOI=10.1006/dbio.1995.1238;
RA Toyama R., Curtiss P.E., Otani H., Kimura M., David I.B., Taira M.;
RT "The LIM class homeobox gene lim5: implied role in CNS patterning in
RT xenopus and zebrafish.";
RL Dev. Biol. 170:583-593 (1995).
RN [2]
RP SEQUENCE OF 188-225 FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Janrich M., Good P.J., David I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
RT specifically in the organizer region of Xenopus gastrula embryos.";
RL Genes Dev. 6:356-366 (1992).
CC -1- FUNCTION: Probably involved in the patterning of the nervous
CC system, in particular in the early specification of the
CC diencephalon.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -1- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; L42546; AAA99464.1; -
DR EMBL; Z11587; CAA77672.1; -
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T04209; -
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeoboxdomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM homeo.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR SMART; SM00389; HOX; 1.

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DR SMART; SM00132; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW Developmental protein; DNA-binding; Homeobox; LIM domain;
KW Metal-binding; Nuclear protein; Repeat; Transcription regulation;
KW Zinc.
FT DOMAIN 3 61 LIM 1.
FT DOMAIN 62 125 LIM 2.
FT DNA_BIND 180 239 Homeobox.
SQ SEQUENCE 402 AA; 44959 MW; A5852B94747E09F9 CRC64;

Query Match      34.2%; Score 55; DB 1; Length 402;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
DB 23 RAWHKVCVQ----CCECKCNLTCK 43

RESULT 44
Q63ZR3
ID Q63ZR3 PRELIMINARY; PRT; 402 AA.
AC Q63ZR3;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.

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```
DR EMBL; BC082847; AAH82847.1; -.
KW Hypothetical protein.
SQ SEQUENCE 402 AA; 44898 MW; 1928D588311BDASB CRC64;

Query Match      34.2%; Score 55; DB 2; Length 402;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
   |::|||::|||::|||
Db 23 RAWHVKCVQ----CCECKCNLTCK 43

RESULT 45
LHX1_XENLA STANDARD; PRT; 403 AA.
ID LHX1_XENLA
AC P29674;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (XLIM-1).
GN Names=LHX1; Synonyms=LIM-1, LIM1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92192449; PubMed=1347750;
RA Taira M., Jamrich M., Good P.J., David I.B.;
RT "The LIM domain-containing homeo box gene Xlim-1 is expressed
RL Genes Dev. 6:356-366(1992).
CC -!- FUNCTION: Probably involved in the establishment of the body plan
CC during gastrulation in embryos.
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- TISSUE SPECIFICITY: In the dorsal LIP and in the dorsal mesoderm
CC as it extend anteriorly (the Spemann's organizer).
CC -!- DEVELOPMENTAL STAGE: Major expression phase at the gastrula stage.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X63889; CAA45353.1; -.
DR PIR; S23802; S23802.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T01962; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; Homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR Pfam; PF00412; LIM; 2.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS0023; LIM_DOMAIN_2; 2.
KW Developmental protein; DNA-binding; Homeobox; LIM domain;
KW Metal-binding; Nuclear protein; Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA_BIND 179 238 Homeobox.
FT
```

```
SQ SEQUENCE 403 AA; 44934 MW; 4147EB3A2774C110 CRC64;

Query Match      34.2%; Score 55; DB 1; Length 403;
Best Local Similarity 44.0%; Pred. No. 69;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNQKCFQHLDDCCSRKCNRFNKC 26
   |::|||::|||::|||
Db 22 RAWHVKCVQ----CCECKCNLTCK 42

RESULT 46
LHX1_HUMAN STANDARD; PRT; 404 AA.
ID LHX1_HUMAN
AC P48742;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE LIM/homeobox protein Lhx1 (Homeobox protein Lim-1).
GN Names=LHX1; Synonyms=LIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97355680; PubMed=9212161;
RA Dong W.F., Heng H.H., Lowsky R., Xu Y., Decoteau J.F., Shi X.-M.,
RA Tsui L.-C., Minden M.D.;
RT "Cloning, expression, and chromosomal localization to 11p12-13 of a
RL DNA Cell Biol. 16:671-678(1997).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC -----
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CC -----
DR EMBL; U14755; AAA21644.1; -.
DR PIR; G01507; G01507.
DR HSSP; P06601; 1FJL.
DR TRANSFAC; T01960; -.
DR Genew; HGNC:6593; LHX1.
DR MIM; 601999; -.
DR GO; GO:0003702; F:RNA polymerase II transcription factor acti. . .; TAS.
DR GO; GO:0007399; P:neurogenesis; TAS.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR001781; LIM.
DR InterPro; IPR007107; LIM_homeo.
DR Pfam; PF00046; Homeobox; 1.
DR Pfam; PF00412; LIM; 2.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000094; LIM; 2.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS0023; LIM_DOMAIN_2; 2.
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA_BIND 180 239 Homeobox.
FT SEQUENCE 404 AA; 44482 MW; CAP2847A340B393F CRC64;
SQ
```

Query Match 34.2%; Score 55; DB 1; Length 404;
 Best Local Similarity 44.0%; Pred. No. 70;
 Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
 | : | | | | | | | | | |
 Db 22 RAWHVRCVQ-----CCECKCNLTCK 42

RESULT 47

LHX1_CHICK
 ID LHX1_CHICK STANDARD; PRT; 406 AA.
 AC P53411;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1).
 GN Name=LHX1; Synonyms=LIM-1, LIM1;
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95094281; PubMed=7528105; DOI=10.1016/0092-8674(94)90027-2;
 RA Tsuchida T., Ensign M., Morton S.B., Baldassare M., Edlund T.,
 RA Jessell T.M., Pfaff S.L.;
 RT "Topographic organization of embryonic motor neurons defined by
 RT expression of LIM homeobox genes.";
 RL Cell 79:957-970(1994).

CC -!- FUNCTION: Transcriptional factor that defines subclasses of
 CC motoneurons that segregate into columns in the spinal cord and
 CC select distinct axon pathways. Acts in conjunction with ISL-2.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- DEVELOPMENTAL STAGE: Expressed prior to the formation of distinct
 CC motor axon pathways and before the segregation of motor neurons
 CC into columns. Expression is confined to the motor neurons in the
 CC lateral subdivision of the lateral motor column (LMC).
 CC -!- SIMILARITY: Contains 1 homeobox domain.
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.

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CC EMBL; L35569; AA62173.1; -;
 CC PIR; I50375; I50375.
 CC HSP; P06601; 1FJL.
 CC InterPro; IPR001356; Homeobox.
 CC InterPro; IPR009057; Homeodomain_like.
 CC InterPro; IPR001781; LIM.
 CC InterPro; IPR007107; LIM_homeo.
 CC Pfam; PF00046; Homeobox; 1.
 CC Pfam; PF00412; LIM; 2.
 CC PRINTS; PR00024; HOMEBOX.
 CC ProDom; PD000010; Homeobox; 1.
 CC ProDom; PD000094; LIM; 2.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 CC PROSITE; PS00478; LIM_DOMAIN 1; 2.
 CC PROSITE; PS50023; LIM_DOMAIN 2; 2.
 CC DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
 CC Repeat; Zinc.
 KW DOMAIN 4 54 LIM 1.
 FT DOMAIN 63 117 LIM 2.
 FT DNA_BIND 180 239 Homeobox.
 FT SEQUENCE 406 AA; 44845 MW; DF1B7BF1F32B9056 CRC64;

Query Match 34.2%; Score 55; DB 1; Length 406;
 Best Local Similarity 44.0%; Pred. No. 70;
 Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26
 | : | | | | | | | | | |
 Db 22 RAWHVRCVQ-----CCECKCNLTCK 42

RESULT 48

LHX1_MESAU
 ID LHX1_MESAU STANDARD; PRT; 406 AA.
 AC P63008; P36199;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Homeobox protein
 DE LMX-2).
 GN Name=Lhx1; Synonyms=Lim-1, Lim1, Lmx2;
 CC Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancratic islets;
 RX MEDLINE=95083670; PubMed=7991607;
 RA Rudnick A., Ling T.Y., Odagiri H., Rutter W.J., German M.S.;
 RA "Pancratic beta cells express a diverse set of homeobox genes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:12203-12207(1994).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- SIMILARITY: Contains 1 homeobox domain.
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.

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CC EMBL; X81407; CAA57164.1; -;
 CC PIR; I48186; I48186.
 CC HSP; P06601; 1FJL.
 CC TRANSFAC; T04264; -;
 CC InterPro; IPR001356; Homeobox.
 CC InterPro; IPR009057; Homeodomain_like.
 CC InterPro; IPR001781; LIM.
 CC InterPro; IPR007107; LIM_homeo.
 CC Pfam; PF00046; Homeobox; 1.
 CC Pfam; PF00412; LIM; 2.
 CC PRINTS; PR00024; HOMEBOX.
 CC SMART; SM00389; HOX; 1.
 CC SMART; SM00132; LIM; 2.
 CC PROSITE; PS00027; HOMEBOX 1; 1.
 CC PROSITE; PS00071; HOMEBOX 2; 1.
 CC PROSITE; PS00478; LIM_DOMAIN 1; 2.
 CC PROSITE; PS50023; LIM_DOMAIN 2; 2.
 CC DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
 CC Repeat; Zinc.
 KW DOMAIN 4 54 LIM 1.
 FT DOMAIN 63 117 LIM 2.
 FT DNA_BIND 180 239 Homeobox.
 FT SEQUENCE 406 AA; 44780 MW; CC8637984998ADAF CRC64;

Query Match 34.2%; Score 55; DB 1; Length 406;
 Best Local Similarity 44.0%; Pred. No. 70;
 Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

QY 2 RIXNOKCFQHLDDCCSRKCNRFNKC 26

```
Db 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42
22 RAWHVQVQ-----CCECKCNLTCK 42

RESULT 49
LHX1 MOUSE
ID LHX1_MOUSE STANDARD; PRT; 406 AA.
AC P63006; P36199;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1).
GN Name=Lhx1; Synonyms=Lim-1, Lim1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=94220754; PubMed=7909459;
RA Fujii T., Pichel J.G., Taira M., Toyama R., Dawid I.B., Westphal H.;
RT "Expression patterns of the murine LIM class homeobox gene lim1 in the
  developing brain and excretory system.";
RL Dev. Dyn. 199;73-83(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94123850; PubMed=7904966; DOI=10.1006/dbio.1994.1018;
RA Barnes J.D., Crosby J.L., Jones C.M., Wright C.V., Hogan B.L.;
RT "Embryonic expression of Lim-1, the mouse homolog of Xenopus Xlim-1,
  suggests a role in lateral mesoderm differentiation and
  neurogenesis.";
RL Dev. Biol. 161;168-178(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvEv;
RX MEDLINE=99269909; PubMed=10337615;
RA Li Y., Cheah S.S., Deng J.M., Shawlot W., Behringer R.R.;
RT "Sequence and genomic organization of the mouse Lim1 gene.";
RL Mamm. Genome 10;444-446(1999).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
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CC EMBL; Z27410; CAA81797.1; -
CC EMBL; S68107; AAC60669.2; -
CC EMBL; AF039706; AAD02169.1; -
CC EMBL; AF039705; AAD02169.1; JOINED.
CC F01; I48637; I48637.
CC HSP; P06601; 1FJL.
CC TRANSFAC; T01961; -
CC MGD; MGI:99783; Lhx1.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR009057; Homeodomain_like.
CC InterPro; IPR001781; LIM.
CC InterPro; IPR007107; LIM homeo.
CC Pfam; PF00046; Homeobox; 1.
CC PRINTS; P00024; HOMEBOX.
CC SMART; SM00389; HOX; 1.
CC SMART; SM00132; LIM; 2.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00478; LIM_DOMAIN_1; 2.
CC PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc.
FT DOMAIN 63 117 LIM 1.
FT DOMAIN 180 239 Homeobox.
FT CONFLICT 12 12 L -> LARQVRPV (in Ref. 2).
FT CONFLICT 24 31 Missing (in Ref. 2).
FT CONFLICT 236 236 R -> A (in Ref. 2).
FT CONFLICT 335 335 H -> HH (in Ref. 2).
SQ SEQUENCE 406 AA; 44780 MW; CC8637984998ADAF CRC64;

Query Match 34.2%; Score 55; DB 1; Length 406;
Best Local Similarity 44.0%; Pred. No. 70;
Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;
QY 2 RIXNQCFQHLDDCCSRKCNRFNKC 26
DB 22 RAWHVQVQ-----CCECKCNLTCK 42

RESULT 50
LHX1 RAT
ID LHX1_RAT STANDARD; PRT; 406 AA.
AC P63007; P36199;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1) (Rlim).
GN Name=Lhx1; Synonyms=Lim-1, Lim1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94336075; PubMed=7914684; DOI=10.1016/0304-3940(94)90334-4;
RA Furuyama T., Inagaki S., Iwahashi Y., Takagi H.;
RT "Distribution of Rlim, an LIM homeodomain gene, in the rat brain.";
RL Neurosci. Lett. 170;266-268(1994).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC EMBL; S71523; AAC60696.1; -
CC HSP; P06601; 1FJL.
CC RGD; 71074; Lhx1.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR009057; Homeodomain_like.
CC InterPro; IPR001781; LIM.
CC InterPro; IPR007107; LIM homeo.
CC Pfam; PF00046; Homeobox; 1.
CC PRINTS; P00024; HOMEBOX.
CC SMART; SM00389; HOX; 1.
CC SMART; SM00132; LIM; 2.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC PROSITE; PS00478; LIM_DOMAIN_1; 2.
CC PROSITE; PS00023; LIM_DOMAIN_2; 2.
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;
KW Repeat; Zinc.
FT DOMAIN 63 117 LIM 1.
FT DOMAIN 180 239 Homeobox.
SQ SEQUENCE 406 AA; 44780 MW; CC8637984998ADAF CRC64;
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Query Match	34.2%	Score 55;	DB 2;	Length 585;
Best Local Similarity	37.9%	Pred. No. 97;		
Matches	11;	Conservative	2;	Mismatches 14;
				Indels

```
Qy 1 CR--IXNQKCFQHLDDCCSKCNRFNKCVCV 27
Db 377 CRAGFAGPRCEHLDLDCAGACANGGTCVCV 405

RESULT 54
Q8NBS4
ID Q8NBS4 PRELIMINARY; PRT; 587 AA.
AC Q8NBS4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90821.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

SEQUENCE FROM N.A.
RA Isegai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
DR EMBL; AK075302; BAC11535.1; -.
DR HSSP; P00740; LEDM.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001005; MYB_DNA_binding.
DR Pfam; PF00008; EGF_5.
DR SMART; SM00181; EGF_6.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 6.
DR PROSITE; PS00334; MYB_2; UNKNOWN_1.
KW EGF-like domain.
SQ SEQUENCE 587 AA; 61144 MW; 2FF5E3EA66789B1B CRC64;

Query Match 34.2%; Score 55; DB 2; Length 587;
Best Local Similarity 37.9%; Pred. No. 97;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 CR--IXNQKCFQHLDDCCSKCNRFNKCVCV 27
Db 379 CRAGFAGPRCEHLDLDCAGACANGGTCVCV 407

RESULT 55
ID DLL3_RAT STANDARD; PRT; 589 AA.
AC O88671;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3).
GN Names=Dll3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Boulter J., Grenfield A., Weinmaster G.;
RT "Rattus norvegicus mRNA for Delta 3: a putative ligand for Notch.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert
neurons along a specific differentiation pathway. Play a role in
```

QY 1 CR--IXNOKCFQHLDDCCSRKCNFNKCV 27
 DB 381 CRAGFAGPRCEHDLDDCAGACANGGTCV 409

RESULT 56
 DLL3 MOUSE
 ID DLL3 MOUSE STANDARD; PRT; 592 AA.
 AC O88516; O35675; O9QWL9; O9QWZ7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Delta-like protein 3 precursor (Drosophila Delta homolog 3) (M-Delta-3).
 DE 3).
 GN Name=Dll3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6 X DBA; TISSUE=Embryo;
 RX MEDLINE=97417575; PubMed=9272948;
 RA Dunwoodie S.L., Henrique D.M.P., Harrison S.M., Beddington R.S.P.;
 RT "Mouse Dll3: a novel divergent Delta gene which may complement the function of other Delta homologues during early pattern formation in the mouse embryo."
 RL Nat. Genet. 19:274-278(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Neural tube;
 RA Nakayama K., Nakayama N., Tomooka Y., Hayashi Y., Takahashi M.;
 RT "Specific expression of a divergent type of Delta in a set of earliest generated neurons including the prospective subplate neurons."
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibits primary neurogenesis. May be required to divert neurons along a specific differentiation pathway. Play a role in the formation of somite boundaries during segmentation of the paraxial mesoderm.
 CC -1- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor (Probable).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=2;
 CC IsoId=O88516-1; Sequence=Displayed;
 CC Name=1;
 CC IsoId=O88516-2; Sequence=VSP_001376;
 CC -1- TISSUE SPECIFICITY: Predominantly expressed in the neuroectoderm and paraxial mesoderm during embryogenesis.
 CC -1- DOMAIN: The DSL domain is required for binding to the Notch receptor.
 CC -1- DISEASE: A truncating mutation in Dll3 is the cause of the pudgy (pu) phenotype. Pudgy mice exhibit patterning defects at the earliest stages of somitogenesis. Adult pudgy mice present severe vertebral and rib deformities.
 CC -1- SIMILARITY: Contains 1 DSL domain.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
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 CC EMBL; AF068865; AAC40170.1; -
 CC EMBL; AF068865; AAC40169.1; -
 CC EMBL; Y11895; CAA72637.1; -
 CC EMBL; AB013440; BAA33716.1; -
 CC HSPB; P00740; IEDM.
 CC MGD; MGI:1096877; Dll3.
 CC GO; GO:0005112; F:Notch binding; NAS.
 CC GO; GO:0001709; P:cell fate determination; NAS.
 CC GO; GO:0007386; P:compartment specification; IMP.
 CC GO; GO:0001701; P:embryonic development (sensu Mammalia); NAS.
 CC GO; GO:0007399; P:neurogenesis; NAS.
 CC GO; GO:0007219; P:Notch signaling pathway; NAS.
 CC GO; GO:0001501; P:skeletal development; IMP.
 CC InterPro; IPR000742; EGF 2.
 CC InterPro; IPR001438; EGF-II.
 CC InterPro; IPR006209; EGF_like.
 CC Pfam; PF00008; EGF; 5.
 CC PRINTS; PRO0010; EGFBLD.
 CC PROSITE; PS00022; EGF 1; 6.
 CC PROSITE; PS01186; EGF 2; 6.
 CC PROSITE; PS00026; EGF 3; 6.
 KW EGF-like domain; Notch signaling pathway; Repeat; Signal;
 KW Transmembrane.
 FT SIGNAL 1 32 Potential.
 FT CHAIN 33 592 Delta-like protein 3.
 FT DOMAIN 33 490 Extracellular (Potential).
 FT TRANSMEM 491 511 Potential.
 FT DOMAIN 512 592 Cytoplasmic (Potential).
 FT DOMAIN 174 213 DSL.
 FT DOMAIN 214 247 EGF-like 1.
 FT DOMAIN 272 308 EGF-like 2.
 FT DOMAIN 310 349 EGF-like 3.
 FT DOMAIN 351 387 EGF-like 4.
 FT DOMAIN 389 425 EGF-like 5.
 FT DOMAIN 427 463 EGF-like 6.
 FT DISULFID 218 229 By similarity.
 FT DISULFID 222 235 By similarity.
 FT DISULFID 237 246 By similarity.
 FT DISULFID 276 287 By similarity.
 FT DISULFID 281 296 By similarity.
 FT DISULFID 298 307 By similarity.
 FT DISULFID 314 325 By similarity.
 FT DISULFID 319 337 By similarity.
 FT DISULFID 339 348 By similarity.
 FT DISULFID 355 366 By similarity.
 FT DISULFID 360 375 By similarity.
 FT DISULFID 377 386 By similarity.
 FT DISULFID 393 404 By similarity.
 FT DISULFID 398 413 By similarity.
 FT DISULFID 415 424 By similarity.
 FT DISULFID 431 442 By similarity.
 FT DISULFID 436 451 By similarity.
 FT DISULFID 453 462 By similarity.
 FT VARSPIC 585 592 DMLIQVLF -> A (in isoform 1).
 FT CONFLICT 94 94 E -> K (in Ref. 3).
 FT CONFLICT 401 401 G -> A (in Ref. 1).
 SQ SEQUENCE 592 AA; 62069 MW; 1A84F8022E7E7DCC CRC64;
 Query Match 34.2%; Score 55; DB 1; Length 592;
 Best Local Similarity 37.9%; Pred. No. 98;
 Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;
 Qy 1 CR--IXNOKCFQHLDDCCSRKCNFNKCV 27
 Db 377 CRAGFAGPRCEHDLDDCAGACANGGTCV 405

```
RESULT 57
DL33_HUMAN
ID D113 HUMAN STANDARD; PRT; 618 AA.
AC Q9NYJ7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Delta-like protein 3 precursor (Drosophila Delta homolog 3).
OS Homo sapiens (Human).
GN Names=DL33;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT SC001 ASP-385.
RX MEDLINE=2026573; PubMed=10742114; DOI=10.1038/74307;
RA Bulman M.P., Kusumi K., Frayling T.M., McKeown C., Garrett C.,
RA Lander E.S., Krulaufer R., Hattersley A.T., Ellard S., Turpenny P.D.,
RT "Mutations in the human delta homologue, DL33, cause axial skeletal
RT defects in spondylocostal dysostosis."
RL Nat. Genet. 24:438-441(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalak U., Smalish D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Inhibits primary neurogenesis. May be required to divert
CC neurons along a specific differentiation pathway. Play a role in
CC the formation of somite boundaries during segmentation of the
CC paraxial mesoderm (By similarity).
CC -!- SUBUNIT: Can bind and activate Notch-1 or another Notch receptor
CC (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- DOMAIN: The DSL domain is required for binding to the Notch
CC receptor.
CC -!- DISEASE: Defects in DL33 are the cause of autosomal recessive
CC spondylocostal dysostosis type 1 (SC001) [MIM:277300]. SC001 is
CC characterized by multiple hemivertebrae, rib fusions and deletions
CC with a non-progressive kyphoscoliosis.
CC -!- SIMILARITY: Contains 1 DSL domain.
CC -!- SIMILARITY: Contains 6 EGF-like domains.
-----
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CC
CC EMBL; AF241373; AAF62542.1; -.
CC EMBL; AF241367; AAF62542.1; JOINED.
CC EMBL; AF241368; AAF62542.1; JOINED.
CC EMBL; AF241369; AAF62542.1; JOINED.
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DR EMBL; AF241370; AAF62542.1; JOINED.
DR EMBL; AF241371; AAF62542.1; JOINED.
DR EMBL; AF241372; AAF62542.1; JOINED.
DR EMBL; BC000218; AAF00218.1; -.
DR HSSP; P00740; LEDM.
DR Genew; HGNC:2909; DLL3.
DR H-INVD; HIX0015121; -.
DR MIM; 602768; -.
DR MIM; 277300; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005112; F:Notch binding; NAS.
DR GO; GO:0001709; P:cell fate determination; ISS.
DR GO; GO:0001701; P:embryonic development (sensu Mammalia); ISS.
DR GO; GO:0007399; P:neurogenesis; ISS.
DR GO; GO:0007219; P:Notch signaling pathway; ISS.
DR GO; GO:0001501; P:skeletal development; IMP.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 5.
DR PRINTS; PR0010; EGFBL00D.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS00026; EGF_3; 6.
DR Developmental protein; Differentiation; Disease mutation; Repeat;
KW EGF-like domain; Notch signaling pathway; Polymorphism; Repeat;
KW Signal; Transmembrane.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 618 Delta-like protein 3.
FT DOMAIN 27 492 Extracellular (Potential).
FT TRANSMEM 493 513 Potential.
FT DOMAIN 514 518 Cytoplasmic (Potential).
FT DOMAIN 176 215 DSL.
FT DOMAIN 216 249 EGF-like 1.
FT DOMAIN 274 310 EGF-like 2.
FT DOMAIN 312 351 EGF-like 3.
FT DOMAIN 353 389 EGF-like 4.
FT DOMAIN 391 427 EGF-like 5.
FT DOMAIN 429 465 EGF-like 6.
FT DISULFID 220 231 By similarity.
FT DISULFID 224 217 By similarity.
FT DISULFID 239 248 By similarity.
FT DISULFID 278 289 By similarity.
FT DISULFID 283 298 By similarity.
FT DISULFID 300 309 By similarity.
FT DISULFID 316 327 By similarity.
FT DISULFID 321 329 By similarity.
FT DISULFID 341 350 By similarity.
FT DISULFID 357 368 By similarity.
FT DISULFID 362 377 By similarity.
FT DISULFID 379 388 By similarity.
FT DISULFID 395 406 By similarity.
FT DISULFID 400 415 By similarity.
FT DISULFID 417 426 By similarity.
FT DISULFID 433 444 By similarity.
FT DISULFID 438 453 By similarity.
FT DISULFID 455 464 By similarity.
FT VARIANT 218 218 L -> P (in dbSNP:1110627).
FT VARIANT 385 385 G -> D (in SC001).
FT VARIANT 385 385 /FTID=VAR_016776.
SQ SEQUENCE 618 AA; 64617 MW; 58A9BC0A7DEAD1A0 CRC64;
Query Match 34.2%; Score 55; DB 1; Length 618;
Best Local Similarity 37.9%; Pred. No. 1e+02;
Matches 11; Conservative 2; Mismatches 14; Indels 2; Gaps 1;
QY 1 CR--IXNQKCFQHLDDCCSRKCNRENKCV 27
||| : ||| |||
Db 379 CRAGFAGPRCEHDLDDCAGRACANGTCV 407
||| : ||| |||
RESULT 58
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Q812A6
ID Q812A6 PRELIMINARY; PRT; 1620 AA.
AC Q812A6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PFA0170C.
GN Name=PFA0170C; Synonym=MA11P1.74b;
OS Plasmodium falciparum (isolate 3D7)
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22255708; PubMed=12368867; DOI=10.1038/nature01095;
RA Hall N., Pain A., Barriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Bucke C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Fellwell T., Goble A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Kontorov B., Kyes S., Larke N., Lawson D., Lennard N.,
RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitz B.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Sulston J.E., Craig A., Newbold C., Barrell B.G;
RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
RL Nature 419:527-531(2002).
DR EMBL; AL031745; CAB48994.1;
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF00246; Peptidase_M14; 1.
KW Hypothetical protein.
SQ SEQUENCE 1620 AA; 19196 MW; 31A7292B814ACE0F CRC64;
Nature 419:527-531(2002).
Query Match 34.2%; Score 55; DB 2; Length 1620;
Best Local Similarity 37.9%; Pred. No. 2.4e+02;
Matches 11; Conservative 5; Mismatches 7; Indels 6; Gaps 1;
QY 4 XNQCQFHLDDCCSRKCNRF-----NKC 26
Db 161 YTNKCQYNDYDYNKCNQYNDYDYNKC 189
[1]
RESULT 59
Q7RR73
ID Q7RR73 PRELIMINARY; PRT; 5309 AA.
AC Q7RR73
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY00634;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carleton J.M., Anguoli S.V., Suh B.B., Kooij T.W., Perteu M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin H.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01000171; EAA17439.1; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR006162; Ppantine S.
DR InterPro; IPR002078; Sig54_interact.
DR PROSITE; PS00012; PHOSPHOPANTHEINE; UNKNOWN_1.
DR PROSITE; PS00675; SIGMAS4_INTERACT_1; 1.
KW Hypothetical protein.
FT NON_TER 5309 5309
SQ SEQUENCE 5309 AA; 628397 MW; 2406AC52CF2F5A93 CRC64;
Query Match 34.2%; Score 55; DB 2; Length 5309;
Best Local Similarity 32.4%; Pred. No. 6.8e+02;
Matches 12; Conservative 5; Mismatches 10; Indels 10; Gaps 2;
QY 1 CR-IXNQCQFQH-----LDDCCSRKCNRFNKC 27
Db 3900 CHIKNESCFTEKQNNVCFEDICKMNVKINKCI 3936
[1]
RESULT 60
CXOA_CONMA
ID CXOA_CONMA STANDARD; PRT; 71 AA.
AC P05484;
DT 01-NOV-1988 (Rel. 09, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Omega-conotoxin MVIIa precursor (SNX-111) (Ziconotide).
OS Conus magus (Magus cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6492;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Venom duct;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes.";
RL J. Biol. Chem. 275:35335-35344(2000).
[2]
RN [2]
RP SEQUENCE OF 46-70.
RX MEDLINE=86070213; PubMed=4071055;
RA Olivera B.M., Gray W.R., Zeikus R.D., McIntosh J.M., Varga J.,
RA Rivier J.E., de Santos V., Cruz L.J.;
RT "Peptide neurotoxins from fish-hunting cone snails.";
RL Science 230:1338-1343(1985).
[3]
RN [3]
RP SEQUENCE OF 46-70.
RX MEDLINE=87299637; PubMed=2441741;
RA Olivera B.M., Cruz L.J., de Santos V., Lechmanant G.W., Griffin D.,
RA Zeikus R.D., McIntosh J.M., Galyean R., Varga J., Gray W.R.,
RA Rivier J.E.;
RT "Neuronal calcium channel antagonists. Discrimination between calcium
RT channel subtypes using omega-conotoxin from Conus magus venom.";
RL Biochemistry 26:2086-2090(1987).
[4]
RN [4]
RP DISULFIDE BONDS.
RX MEDLINE=96122182; PubMed=8537186;
RA Chung D., Gaur S., Bell J.R., Ramachandran J., Nadasdi L.;
RT "Determination of disulfide bridge pattern in omega-conopeptides.";
RL Int. J. Pept. Protein Res. 46:320-325(1995).
[5]
RN [5]

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723711; AAU21452.1; -
 SQ SEQUENCE 74 AA; 7825 MW; 537318AAFF612545 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 74;
 Best Local Similarity 37.0%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;
 QY 7 KCFQHLDD-----DCCSRKCNRFNK 26
 DB 45 KCCQAINADPIAFHDCCKSCNCTGSPC 71

RESULT 63

Q646W1
 ID Q646W1 PRELIMINARY; PRT; 74 AA.
 AC Q646W1;
 DT 25-OCT-2004 (TremBLrel. 28, Created)
 DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
 DE Phytoxin-like SCR74.
 OS Phytophthora infestans (Potato late blight fungus)
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora
 OC NCBI_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
 RA Torto-Alalibo T., Min J., Avrova A.O., Wright F., Birch P.R.J.,
 RA Kamoun S.;
 RT "Patterns of Diversifying Selection in the Phytoxin-like scr74 Gene
 RT Family of Phytophthora infestans";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY723705; AAU21446.1; -
 SQ SEQUENCE 74 AA; 7885 MW; 98D110005D613927 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 74;
 Best Local Similarity 37.0%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 6; Indels 7; Gaps 1;
 QY 7 KCFQHLDD-----DCCSRKCNRFNK 26
 DB 45 KCCQAINADPIAFHDCCKSCNCTGSPC 71

RESULT 64

O18052
 ID O18052 PRELIMINARY; PRT; 247 AA.
 AC O18052;
 DT 01-JAN-1998 (TremBLrel. 05, Created)
 DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Hypothetical protein T06G6.6.
 GN ORFNames=T06G6.6;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C.elegans: A platform for
 RT investigating biology.";
 RL Science 282:2012-2018 (1998).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Kershaw J.K.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81587; CAB04705.2; -
 WormBase; WBGene00011548; T06G6.6.

DR WormPep; T06G6.6; CE13343.
 KW Hypothetical protein.
 SQ SEQUENCE 247 AA; 27954 MW; 26FAB589C121PBEB CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 247;
 Best Local Similarity 33.3%; Pred. No. 52;
 Matches 10; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 3 IXNOKCFQHLDD-----DCCSRKCNRFNK 25
 DB 77 INDNGCFMHFDKSKLESIELCLPQCFNE 106

RESULT 65

Q97GL5
 ID Q97GL5 PRELIMINARY; PRT; 252 AA.
 AC Q97GL5;
 DT 01-OCT-2001 (TremBLrel. 18, Created)
 DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
 DE Glycosyltransferase.
 GN OrderedLocusNames=CAC2351;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OC NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R.L., Lee H.M., Dubois J., Glu D., Hitti J., Wolf Y.I.,
 RA Tatsov R., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum";
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL; AE007735; AAK80307.1; -
 DR FIR; H97189; H97189.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR001173; Glyco trans 2.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 252 AA; 29892 MW; C7A45BA39F534DE9 CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 252;
 Best Local Similarity 37.0%; Pred. No. 53;
 Matches 10; Conservative 5; Mismatches 5; Indels 7; Gaps 2;
 QY 3 IXNOKCFQHLDDCCSR-----KCNRFN 24
 DB 188 LAEDACF--IEDCKQGIKIYSCNRFN 212

RESULT 66

O18720
 ID O18720 PRELIMINARY; PRT; 1282 AA.
 AC O18720;
 DT 01-JAN-1998 (TremBLrel. 05, Created)
 DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE Gal/GalNAc-inhibitable adherence lectin.
 GN Name=dhgl2;
 OS Entamoeba dispar.
 OC Eukaryota; Entamoebidae; Entamoeba.
 OC NCBI_TaxID=46681;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAW760;
 RX MEDLINE=97376907; PubMed=9233678; DOI=10.1016/S0166-6851(97)00047-9;
 RA Pillai D.R., Britten D., Ackers J.P., Ravdin J.I., Kain K.C.;
 RT "A gene homologous to hgl2 of Entamoeba histolytica is present and
 RT expressed in Entamoeba dispar.";

```
RL Mol. Biochem. Parasitol. 87:101-105(1997).
DR EMBL; U73710; AAC47580.1; -.
DR GO; GO:0005529; F: eugarg binding; IEA.
DR InterPro; IPR006209; EGF like.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
KW Lectin.
SQ SEQUENCE 1282 AA; 143481 MW; 48BD2FA64140C33E CRC64;

Query Match 33.9%; Score 54.5; DB 2; Length 1282;
Best Local Similarity 38.8%; Pred. No. 2.2e+02;
Matches 11; Conservative 4; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNQKCFQHLDDCCSRK--CNRFN-KC 26
DB 708 CSMGTDNVISYCEDCASRKSQCQGNFGKC 736

RESULT 67
CXOD_CONCT STANDARD; PRT; 73 AA.
AC PS8920;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Omega-conotoxin CVID precursor.
OS Conus catus (Cat cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 46-72, SYNTHESIS, AND STRUCTURE BY
RP NNR.
RC TISSUE=Venom, and Venom duct;
RX MEDLINE=20519630; PubMed=10938268; DOI=10.1074/jbc.M002252200;
RA Lewis R.J., Nielsen K.J., Craik D.J., Loughnan M.L., Adams D.A.,
RA Sharpe I.A., Luchian T., Adams D.J., Bond T., Thomas L., Jones A.,
RA Matheson J.-L., Drinkwater R., Andrews P.R., Alewood P.F.;
RT "Novel omega-conotoxins from Conus catus discriminate among neuronal
RT calcium channel subtypes."
RL J. Biol. Chem. 275:35335-35344 (2000).
CC -!- FUNCTION: Omega-conotoxins act at presynaptic membranes, they bind
CC and block voltage-sensitive calcium channels (VSCC) (By
CC similarity). This toxin blocks N-type calcium channels.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin O-superfamily. Omega-type
CC family.
DR HSSP; P05484; 1DW4.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
KW Amidation; Calcium channel inhibitor; Direct protein sequencing;
KW Ionic channel inhibitor; Neurotoxin; Presynaptic neurotoxin; Signal;
KW Toxin.
FT SIGNAL 1 22 Potential.
FT PROPEP 23 45
FT PEPTIDE 46 72 Omega-conotoxin CVID.
FT DISULFID 46 61 By similarity.
FT DISULFID 53 65 By similarity.
FT DISULFID 60 72 By similarity.
FT MOD_RES 72 72 Cysteine amide (G-73 provides amide
FT group).
SQ SEQUENCE 73 AA; 7748 MW; C4CEBD30C77DAEC3 CRC64;

Query Match 33.5%; Score 54; DB 1; Length 73;
Best Local Similarity 38.8%; Pred. No. 20;
Matches 8; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 1 CRXNQKCFQHLDDCCSRKN 21
DB 46 CKSGAKCSKLMYDCCSGSCS 66

RESULT 68
ID Q80LT7 PRELIMINARY; PRT; 247 AA.
AC Q80LT7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Adoxophyes honmai nucleopolyhedrovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=224399;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ADN001;
RX MEDLINE=22963401; PubMed=14599801; DOI=10.1016/j.virol.2003.08.002;
RA Nakai M., Goto C., Kang W., Shikata M., Luque T., Kunimi Y.;
RT "Genome sequence and organization of a nucleopolyhedrovirus isolated
RT from the smaller tea tortrix, Adoxophyes honmai."
RL Virology 316:171-183(2003).
DR EMBL; AF006270; BAC67260.1; -.
KW Hypothetical protein.
SQ SEQUENCE 247 AA; 28773 MW; 9E53E54D3E022C25 CRC64;

Query Match 33.5%; Score 54; DB 2; Length 247;
Best Local Similarity 40.7%; Pred. No. 60;
Matches 11; Conservative 3; Mismatches 9; Indels 4; Gaps 1;

QY 4 XNQKCFQ----HLDDCCSRKCNRFNKC 26
DB 168 CEKKCFAPRLHDLGLVCDKCGYNFC 194

RESULT 69
LHX1_BRARE STANDARD; PRT; 405 AA.
ID LHX1_BRARE
AC Q90476;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE LIM/homeobox protein Lhx1 (Homeobox protein LIM-1).
GN Name=Lhx1a; Synonyms=lhx1, lim1;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gastrula, and Neurula;
RX MEDLINE=95285760; PubMed=7768180;
RA Toyama R., O'Connell M.L., Wright C.V.E., Kuehn M.R., Dawid I.B.;
RT "Nodal induces ectopic goosecoid and lim1 expression and axis
RT duplication in zebrafish."
RL Development 121:383-391(1995).
CC -!- FUNCTION: Seems to play a role in dorsal axis formation.
CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- DEVELOPMENTAL STAGE: Detected 4 hours after fertilization, maximum
CC levels are seen in 6-hours embryos. Expression then declines
CC during gastrulation (6-10 hours), but is still detectable in 24-
CC and 30-hours embryos. The spatial distribution also vary during
CC embryogenesis: at the beginning, expression is localized in deep
CC cells, and absent from the enveloping layer. The pattern then
CC becomes asymmetric, restricted to the forming embryonic shield. By
CC the shield stage, it is highly localized in the axial hypoblast.
CC As gastrulation proceeds, expression still continues in the
CC involuting cells, extending from the margin towards the anterior.
CC -!- SIMILARITY: Contains 1 homeobox domain.
CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC EMBL; J37802; AAA92157.1; -.
CC HSSP; P06601; 1FJL.
CC ZFIN; ZDB-GENE-980526-347; lhx1a.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR009057; Homeobox_domain_like.
CC InterPro; IPR001781; LIM.
CC InterPro; IPR007107; LIM homeo.
CC Pfam; PF00046; Homeobox; 1.
CC PRINTS; PR00412; LIM; 2.
CC ProDom; PD000010; Homeobox; 1.
CC ProDom; PD000094; LIM; 2.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS00071; HOMEBOX 2; 1.
CC PROSITE; PS00478; LIM DOMAIN 1; 2.
CC PROSITE; PS00023; LIM DOMAIN 2; 2.
CC Developmental protein; DNA-binding; Homeobox; LIM domain;
KW Metal-binding; Nuclear protein; Repeat; Zinc.
FT DOMAIN 4 54 LIM 1.
FT DOMAIN 63 117 LIM 2.
FT DNA BIND 179 238 Homeobox.
SQ SEQUENCE 405 AA; 45153 MW; 186EBEB59C88123 CRC64;

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Query Match 33.5%; Score 54; DB 1; Length 405;
 Best Local Similarity 44.0%; Pred. No. 93;
 Matches 11; Conservative 2; Mismatches 8; Indels 4; Gaps 1;

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Qy 2 RIXNQKCFQHLDDCCSRKCNRFNK 26
Db 22 RAWHIKCVQ---CCECKNLTEKC 42

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RESULT 70

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ID 045117 PRELIMINARY; PRT; 552 AA.
AC 045117;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ultraspiracle.
GN Name=USP-1;
OS Chironomus tentans (Midge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99457719; PubMed=10528412; DOI=10.1016/S0965-1748(99)00068-5;
RA Vogtli M., Imhof M.O., Brown N.E., Rauch P., Spindler-Barth M.,
RA Lezzi M., Henrich V.C.;
RT "Functional characterization of two Ultraspiracle forms (CtUSP-1 and
RT CtUSP-2) from Chironomus tentans.";
RL Insect Biochem. Mol. Biol. 29:931-942(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Vogtli M.O., Henrich V.C., Imhof M.O., Lezzi M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBSJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family.
DR EMBL; AF045891; AAC03056.1; -.
DR HSSP; P20153; 1R00.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005496; F:steroid binding; IEA.
DR GO; GO:0003707; F:steroid hormone receptor activity; IEA.
DR GO; GO:0003700; F:steroid hormone receptor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000536; Hrmn_recept_lig.

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DR InterPro; IPR000003; RtnoidX_receptor.
DR InterPro; IPR001723; Stdhrm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; Hormone_recep; 1.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR00545; RETINOIDXR.
DR PRINTS; PR00398; STRDHORMONER.
DR PRINTS; PR00047; STROIDDFINGER.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
KW Transcription regulation; Zinc; Zinc-finger.
SQ SEQUENCE 552 AA; 61882 MW; 3261341C2BD0A98E CRC64;

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Query Match 33.5%; Score 54; DB 2; Length 552;
 Best Local Similarity 40.0%; Pred. No. 1.2e+02;
 Matches 10; Conservative 6; Mismatches 7; Indels 2; Gaps 1;

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Qy 1 CRXNQKCFQHLDDCCSRKCNRFNK 25
Db 345 CAMVKNQVFQHMDFC--RLPHFTK 367

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RESULT 71

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Q68KF8 PRELIMINARY; PRT; 911 AA.
ID Q68KF8;
AC Q68KF8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Subtilisin-like protease SPC6A.
GN Name=spc6a;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas J.T., Weih K.A., Prakash D., Moos M. Jr.;
RT "Vgl and CDMF-1/GDF5 Have Specific Processing Requirements That
RT Restrict their Sites of Action to Body Axis and Joint Patterning
RT Centers.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY685229; AAT99305.1; -.
GO; GO:0008233; F:peptidase activity; IEA.
DR InterPro; IPR006212; Furin_repeat.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR006210; IEGF_
DR InterPro; IPR000209; Rept_S8_S53.
DR InterPro; IPR009020; Prot_inh_propt.
DR InterPro; IPR002884; Prototnconvertsp.
DR Pfam; PF00082; Peptidase_S8; 1.
DR Pfam; PF01483; P_protein; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR ProDom; PD000717; Prototnconvertsp; 1.
DR SMART; SM00181; EGF; 4.
DR SMART; SM00261; FU; 5.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE_SER; 1.
KW Protease.
SQ SEQUENCE 911 AA; 101427 MW; E75C63CB60D3B82F CRC64;

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Query Match 33.5%; Score 54; DB 2; Length 911;
 Best Local Similarity 38.1%; Pred. No. 1.9e+02;
 Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

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Qy 6 QKCFQHLDDCCSRKCNRFNK 26
Db 683 KKCFCQHCDCVGSRTDQCTAC 703

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RESULT 72
P91526 PRELIMINARY; PRT; 1372 AA.
AC P91526;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein W02C12.1.
GN Names=W02C12.1; ORFNames=W02C12.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99089613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Murray J., Wohlmann P.;
RT "The sequence of C. elegans cosmid W02C12."
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RG WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80815; AAB37995.1; -.
DR PIR; T25933; T25933.
DR HSSP; Q12780; IHAE.
DR WormBase; WBGene00020928; W02C12.1.
DR WormPep; W02C12.1; CEI4412.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_III.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR003410; HyalIn.
DR InterPro; IPR001759; Pentaxin.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 10.
DR Pfam; PF02494; HYR; 1.
DR PRINTS; PR00010; EGFBL00D.
DR ProDom; PD002153; Pentaxin; 1.
DR SMART; SM00032; CCP; 1.
DR SMART; SM00179; EGF_CA; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 5.
DR PROSITE; PS00022; EGF_1; 11.
DR PROSITE; PS01186; EGF_2; 8.
DR PROSITE; PS00026; EGF_3; 12.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00825; HYR; 1.
DR PROSITE; PS0923; SUSHI; 1.
KW EGF-like domain; Hypothetical protein.
SQ SEQUENCE 1372 AA; 150561 MW; 0537FA79BA0576C5 CRC64;
```

Query Match 33.5%; Score 54; DB 2; Length 1372;
Best Local Similarity 29.2%; Pred. No. 2.7e+02;

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Matches 7; Conservative 7; Mismatches 10; Indels 0; Gaps 0;
QY 4 XNQKCFQHLDDCCSRKCNRFNRCV 27
Db 95 TGENCDQNDIECAASPCQNDAKCI 118
RESULT 73
Q9DE37 PRELIMINARY; PRT; 1515 AA.
AC Q9DE37;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Slit3.
GN Name=slit3;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Michigan;
RX MEDLINE=21098742; PubMed=11161558; DOI=10.1006/dbio.2000.0105;
RA Yeo S.Y., Little M.H., Yamada T., Miyashita T., Halloran M.C.,
RA Kuwada J.Y., Huh T.L., Okamoto H.;
RT "Overexpression of a slit homologue impairs convergent extension of
the mesoderm and causes cyclopia in embryonic zebrafish.";
RL Dev. Biol. 230:1-17(2001).
DR EMBL; AF210320; AAG36772.1; -.
DR HSSP; P01132; 1GK5.
DR ZFIN; ZDB-GENE-010306-4; slit3.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003645; FOL_N.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR003129; TSP_N.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF02210; Laminin_G_2; 1.
DR Pfam; PF01463; LRRCT; 4.
DR Pfam; PF01462; LRRNT; 4.
DR Pfam; PF00560; LRR_1; 19.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00041; CT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00274; FOLN; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00082; LRRCT; 4.
DR SMART; SM00013; LRRNT; 4.
DR PROSITE; PS00369; LRR_Typ; 9.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01185; CTCK_1; UNKNOWN_1.
DR PROSITE; PS01225; CTCK_2; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 7.
DR PROSITE; PS00026; EGF_3; 8.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00025; LAM_G_DOMAIN; 1.
KW EGF-like domain.
SQ SEQUENCE 1515 AA; 166871 MW; 12FD111277D18D5B CRC64;
```

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Query Match      33.5%; Score 54; DB 2; Length 1515;
Best Local Similarity 37.5%; Pred. No. 3e+02;
Matches 9; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY      4 XNOKCFQHLDDCCSRKCNRFNKC 27
DB      1059 VQCCFQDYNDCLNKCQHGACV 1082

RESULT 74
HSPC_ELECI
ID      HSPC_ELECI      STANDARD;      PRT;      84 AA.
AC      P83183;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Cysteine-rich protamine.
OS      Eleione cirrhosa (Curled octopus) (Ozaena cirrhosa).
OC      Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Naucoroidea;
OC      Octopodiformes; Octopoda; Incirrata; Octopodidae; Eleione.
OX      NCBI_TaxID=102876;
RN      [1]
RP      SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC      TISSUE-Sperm;
RX      MEDLINE=22108191; PubMed=12113475;
RA      Gimenez-Bonafe P., Ribes E., Sautiere P., Gonzalez A., Kasinsky H.E.,
RA      Kouach M., Sautiere P.-E., Ausio J., Chiva M.;
RT      "Chromatin condensation, cysteine-rich protamine, and establishment of
RT      disulphide interprotamine bonds during spermiogenesis of Eleione
RT      cirrhosa (Cephalopoda).";
RL      Eur. J. Cell Biol. 81:341-349 (2002).
CC      -!- FUNCTION: Protamines substitute for histones in the chromatin of
CC      sperm during the haploid phase of spermatogenesis. They compact
CC      sperm DNA into a highly condensed, stable and inactive complex.
CC      This protamine condenses spermiogenic chromatin in a pattern which
CC      comprises fibres with a progressively larger diameter and lamellae
CC      that finally undergo definitive coalescence.
CC      -!- SUBUNIT: Cross-linked by interchain disulfide bonds around the
CC      DNA-helix (By similarity).
CC      -!- SUBCELLULAR LOCATION: Nuclear.
CC      -!- TISSUE SPECIFICITY: Testis.
DR      InterPro: IPR001212; Somatomedin B.
KW      Chromosomal protein; Direct protein sequencing; DNA condensation;
KW      DNA-binding; Nuclear protein; Nucleosome core; Spermatogenesis.
FT      DISULFID 12 12 Interchain (with C-31) (By similarity).
FT      DISULFID 16 24 By similarity.
FT      DISULFID 31 31 Interchain (with C-12) (By similarity).
FT      DISULFID 63 63 Interchain (with C-63) (By similarity).
FT      DISULFID 64 80 By similarity.
SQ      SEQUENCE 84 AA; 10612 MW; 70932DAC3C71837E CRC64;

Query Match      33.2%; Score 53.5; DB 1; Length 84;
Best Local Similarity 31.0%; Pred. No. 27;
Matches 9; Conservative 7; Mismatches 10; Indels 3; Gaps 1;

QY      1 CRXNOKCFQHLDDCCSRK---CNRFNKC 26
DB      24 CRRCRRCRSRIVKCCRRRSCCRRRRRC 52

RESULT 75
Q693N8
ID      Q693N8      PRELIMINARY;      PRT;      476 AA.
AC      Q693N8;
DT      25-OCT-2004 (TREMBLrel. 28, Created)
DT      25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE      3-hydroxy-3-methylglutaryl-CoA synthase (EC 2.3.3.10).
DE      Taxus x media.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX      NCBI_TaxID=85957;
RN      [1]
```

```
SEQUENCE FROM N.A.
Kai G., Miao Z., Tang K.;
"Cloning and expression analyses of a new gene encoding 3-hydroxy-3-
methylglutaryl-CoA synthase from Taxus x media.";
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY644708; AAT73206.1; -.
GO; GO:0008415; F:acetyltransferase activity; IEA.
GO; GO:0016740; F:hydroxymethylglutaryl-CoA synthase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
InterPro: IPR008260; HMG-CoA synth.
InterPro: IPR010122; HMG-CoA synth.
PFam: PF01154; HMG-CoA synt; 1.
TIGRFAMs: TIGR01833; HMG-CoA-S_euk; 1.
Acyltransferase; Transferase.
SQ      SEQUENCE 476 AA; 52863 MW; 973883623142EE0D CRC64;

Query Match      33.2%; Score 53.5; DB 2; Length 476;
Best Local Similarity 43.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

QY      4 XNOKCF-QHLDDCCSRKCNRFNKC 25
DB      211 LSQTCYLKALDSCYKRFNCFK 233

RESULT 76
NH25_CAEEL
ID      NH25_CAEEL      STANDARD;      PRT;      572 AA.
AC      Q19345; Q9NJ95; Q9NJ96; Q9NJ97;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DE      Nuclear hormone receptor family member nhr-25.
GN      Name=nhr-25; ORFNames=F11C1.6;
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.
RC      STRAIN=Bristol N2;
RX      MEDLINE=20237592; PubMed=1072806; DOI=10.1006/dbio.2000.9679;
RA      Gisendanner C.R., Sludner A.E.;
RT      "nhr-25, the Caenorhabditis elegans ortholog of ftz-fl, is required
RT      for epidermal and somatic gonad development.";
RL      Dev. Biol. 221:259-272 (2000).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RX      MEDLINE=99069613; PubMed=9851916;
RG      The C. elegans sequencing consortium;
RT      "Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology.";
RL      Science 282:2012-2018 (1998).
CC      -!- FUNCTION: Orphan nuclear receptor. Seems to be required during
CC      development. Disruption of nhr-25 function leads to embryonic
CC      arrest due to failure of the epidermally mediated process of
CC      embryo elongation.
CC      -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=Alpha;
CC      IsoId=Q19345-1; Sequence=Displayed;
CC      Name=Beta;
CC      IsoId=Q19345-2; Sequence=VSP_003723;
CC      -!- TISSUE SPECIFICITY: Expressed in the epidermis, the developing
CC      somatic gonad, and a subset of other epithelial cells.
CC      -!- SIMILARITY: Belongs to the nuclear hormone receptor family.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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DR ENBL; AF179214; AAF67038.1; -
 DR ENBL; AF179215; AAF67039.1; -
 DR ENBL; AF179216; AAF67040.1; -
 DR ENBL; Z54270; CAA91028.1; -
 DR PIR; T20764; T20764.
 DR HSP; P19793; 2NL.
 DR WormBase; WBGene0003623; F11C1.6.
 DR WormPep; F11C1.6; CE03191.
 DR InterPro; IPR00536; Hmon_recept_lig.
 DR InterPro; IPR001723; Stdhrmn_receptor.
 DR InterPro; IPR008946; Str_ncl_receptor.
 DR InterPro; IPR000324; VitD_receptor.
 DR InterPro; IPR001628; Znf_C4steroid.
 DR Pfam; PF00104; Hormone_recep; 1.
 DR Pfam; PF00105; zf-C4; 1.
 DR PRINTS; PR00398; STRDHORMONER.
 DR PRINTS; PR00047; STROIDFINGER.
 DR PRINTS; PR00350; VITAMINDR.
 DR ProDom; PD000035; Znf_C4steroid; 1.
 DR SMART; SM00430; HOL1; 1.
 DR SMART; SM00399; Znf_C4; 1.
 DR PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
 KW Alternative splicing; Developmental protein; DNA-binding;
 KW Nuclear protein; Receptor; Transcription regulation; Zinc-finger.
 FT DNA_BIND 18 83
 FT ZN_FING 18 38
 FT ZN_FING 54 78
 FT VARSPLIC 1 80
 FT Missing (in Isoform Beta).
 FT /FTID=VSP_003723.
 FT CONFLICT 100 100 F -> L (in Ref. 2; AAF67039).
 FT CONFLICT 540 540 R -> Q (in Ref. 2; AAF67039).
 SQ SEQUENCE 572 AA; 64772 MW; D3092AES33092D7A CRC64;
 Query Match 33.2%; Score 53.5; DB 1; Length 572;
 Best Local Similarity 32.4%; Pred. No. 1.4e+02;
 Matches 11; Conservative 8; Mismatches 6; Indels 9; Gaps 2;
 QY 3 IXNQKCFQ-----HLDDCCSRKCN--RFNKC 27
 Db 46 VQNKQVQCSAEANCHVDRTCKRCPCRCFOKCL 79
 RESULT 77
 ID ITXA_PANIM STANDARD; PRT; 33 AA.
 AC P59868;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Imperatoxin A (ipTxa) (Imperatoxin activator).
 OS Pandinus imperator (Emperor scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Urida; Scorpionioidea; Scorpionidae; Scorpioninae; Pandinus.
 OX NCBI_TaxID=55084;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=97261909; PubMed=9108323; DOI=10.1016/S0014-5793(97)00227-5;
 RA Zamudio F.Z., Gurrola G.B., Arevalo C., Sreekumar R., Walker J.W.,
 RA Valdivia H.H., Possani L.D.;
 RT "Primary structure and synthesis of Imperatoxin A (IpTx(a)), a peptide
 RT activator of Ca2+ release channels/ryanodine receptors.";
 RL FEBS Lett. 405:385-389 (1997).
 RN [2]
 RP IDENTIFICATION.
 RX MEDLINE=93101692; PubMed=1334561;
 RA Valdivia H.H., Kirby M.S., Lederer W.J., Coronado R.;
 RT "Scorpion toxins targeted against the sarcoplasmic reticulum Ca(2+)-

RT release channel of skeletal and cardiac muscle.";
 RN Proc. Natl. Acad. Sci. U.S.A. 89:12185-12189 (1992).
 RL [3]
 RP FUNCTION ON RYR1 AND RYR2.
 RX MEDLINE=98232523; PubMed=9565405;
 RA Tripathy A., Resch W., Xu L., Valdivia H.H., Meissner G.;
 RT "Imperatoxin A induces subconductance states in Ca2+ release channels
 RT (ryanodine receptors) of cardiac and skeletal muscle.";
 RL J. Gen. Physiol. 111:679-690 (1998).
 RN [4]
 RP FUNCTION ON RYR3.
 RX MEDLINE=21855933; PubMed=11867448;
 RA Nabhani T., Zhu X., Simeoni I., Sorrentino V., Valdivia H.H.,
 RA Garcia J.;
 RT "Imperatoxin A enhances Ca(2+) release in developing skeletal muscle
 RT containing ryanodine receptor type 3.";
 RL Biophys. J. 82:1319-1328 (2002).
 CC -1- FUNCTION: Strong agonist of ryanodine receptors (calcium release
 CC channels). Induces voltage- and concentration-dependent
 CC subconductance states in both skeletal (RYR1 and RYR3) and cardiac
 CC (RYR2) ryanodine receptors by binding to a single, cytosolically
 CC accessible site different from the ryanodine binding site.
 CC Enhances calcium release.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- SIMILARITY: Belongs to the scorpion calcine family.
 KW Calcium channel inhibitor; Direct protein sequencing;
 KW Ionic channel inhibitor; Neurotoxin; Toxin.
 FT DISULFID 3 17 By similarity.
 FT DISULFID 10 21 By similarity.
 FT DISULFID 16 32 By similarity.
 SQ SEQUENCE 33 AA; 3764 MW; D0DF8EFFE294537 CRC64;
 Query Match 32.9%; Score 53; DB 1; Length 33;
 Best Local Similarity 42.9%; Pred. No. 13;
 Matches 9; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 QY 8 CFQHL-----DDCCSRKCN 22
 Db 3 CLPFLKRCRKADNDCGKCKR 23
 RESULT 78
 Q8YXK8
 ID Q8YXK8; PRELIMINARY; PRT; 85 AA.
 AC Q8YXK8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein CPE1386.
 GN OrderedLocusNames=CPE1386;
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13;
 RX MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799;
 RA Shimizu T., Ohtani K., Hirakawa H., Onshima K., Yamashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001 (2002).
 DR EMBL; AF003190; BAB81092.1; -
 DR PRINTS; PR00003; 4DISULPHCORE.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 85 AA; 9440 MW; 90EA03381B8D681 CRC64;
 Query Match 32.9%; Score 53; DB 2; Length 85;
 Best Local Similarity 37.5%; Pred. No. 31;
 Matches 12; Conservative 5; Mismatches 9; Indels 6; Gaps 2;

Qy	1	CRXNQ-KCFQHLDDCSRK-----CNHFNKC	26
		: : :	
Db	11	CRCKCECKCKGKXHDCCSQSRNTGCSGFNAC	42

RESULT 79

Q6LZL1	
ID	PRELIMINARY; PRT; 191 AA.
AC	Q6LZL1
AC	Q6LZL1;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Related to iron-sulfur flavoprotein of Methanoscarchina thermophila.
DE	
GN	OrderedLocusNames=MWP0614;
GN	Methanococcus maripaludis.
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC	Methanococcaceae; Methanococcus.
OX	NCBI_TaxID=39152;
RP	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=S2 / LL;
RC	Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J.,
RA	Conway de Macario E., Dodsworth J., Gillett W., Graham D.E.,
RA	Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T.,
RA	Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G.,
RA	Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V.,
RA	Leigh J.A.;
RT	"Complete genome sequence of the mesophilic hydrogenotrophic
RT	methanogen Methanococcus maripaludis.";
RL	Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BX957220; CAF30170.1; "
DR	InterPro; IPR005025; FMN_red.
DR	Pfam; PF03358; FMN_red; I.
KW	Complete proteome.
Q6LZL1	SEQUENCE 191 AA; 21019 MW; BCF6A6F188DF7163 CRC64;

Query Match 32.9%; Score 53; DB 2; Length 191;
Best Local Similarity 38.1%; Pred. No. 63;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 7 KCFQHLDCCSRKCNRFNKCv 27
|||:|::|:|:|:|:
Db 52 KCFETLNNKCIIECDIINNcI 72

RESULT 80

Q7XZ30		PRELIMINARY,	PRT;	225 AA.
ID	Q7XZ30			
AC	Q7XZ30;			
DI	01-OCT-2003 (TREMBLrel. 25, Created)			
DE	01-OCT-2003 (TREMBLrel. 25, Last sequence update)			
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Norch-like protein la (Fragment).			
OC	Griffithsia japonica (Red alga).			
OC	Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Ceramiaceae; Griffithsia.			
NCBI_TaxID=83288;				
[1]	SEQUENCE FROM N.A.			
RPN	Liu C.L., Lee Y.K., Lee H.K.;			
RRR	Submitted (JUN-2002) to the EMBL/GenBank/DBDJ databases.			
OR	EMBL; AY123122; AAM933994.1; -			
FT	NON_TER	225		
FO	SEQUENCE	225 AA;	25897 MW;	1D93A3AA1531DD058 CRC64:

Query Match 32.9%; Score 53; DB 2; Length 225;
Best Local Similarity 41.4%;
Pred. No. 73;
Matches 12; Conservative 4; Mismatches 5; Indels

7 KCFQHLDDC--CS--RKN-----RFNKC 27
168 ECFPKDDCETCSKDCKSGDCRYNKCI 196

RESULT 81

Q86152	PRELIMINARY;	PRT;	234 AA.
ID	Q86152		
AC	Q86152;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein.		
DE	Hypothetical protein.		
OS	Dictyostellium discoideum (Slime mold).		
OX	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.		
OC	NCBI_TaxId=44689;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AX4.		
RC	STRAIN=AX4;		
RC	MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;		
RA	Gloeckner G., Eichinger L., Safranski K., Pachebat J., D��ar P.,		
RA	Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,		
RA	Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;		
RT	"Sequence and analysis of chromosome 2 of Dictyostellium discoideum."		
RT	Nature 418:79-85(2002).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AX4;		
RC	STRAIN=AX4;		
RA	Baumgart C.;		
RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AC116305; AA052288.1; -.		
KW	Hypothetical protein.		
SK	SEQUENCE 234 AA; 27944 MW; BB426ECDAF9B3032 CRC64;		
SQ			

Query Match 32.9%; Score 53; DB 2; Length 234;
Best Local Similarity 40.0%; Pred. No. 76;
Matches 10; Conservative 6; Mismatches 7; Indels

QY 3 IXNQKCF--QHLDDCCSPKCNRFNK 25
|:|:| | :|:|:| | :|:|
Db 36 ITNENIFKNYLNKCCNCKINNYNK 60

RESULT 82

023297	PRELIMINARY;	PRT;	277 AA.
023297			
01-JAN-1998	(TrEMBLrel. 05, Created)		
01-JAN-1998	(TrEMBLrel. 05, Last sequence update)		
05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein dl3245w (Hypothetical protein AT4g14410)		
DE	(Putative bHLH transcription factor).		
DE	Name=dl3245w; Synonyms=AT4g14410;		
GN	Arabidopsis thaliana (Mouse-ear cress).		
GN	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;		
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.		
OC	[1]		
NCBI_TaxID=3702;			
GN	SEQUENCE FROM N.A.		
RP	Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terryn N.,		
RA	Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,		
RA	Puigdomenech P., Hatzipoulos P., Obermaier B., Duesterhoft A.,		
RA	Jones J., Palme K., Ansoerge W., Delsen M., Bancroft I., Mewes H.W.,		
RA	Schuelter C., Chalhazis N.,		
RA	Schuelter C. (2001-1997) to the EMBL/GenBank/DBJ databases		

SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

P
P
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SEQUENCE FROM N.A.
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
[4]
SEQUENCE FROM N.A.
P
P

RC TISSUE=whole plant;
RX MEDLINE=22598051; PubMed=12679534; DOI=10.1093/molbev/meg088;
RA Heim M.A., Jakoby M., Werber M., Martin C., Weissshaar B., Bailey P.C.;
RT "The basic helix-loop-helix transcription factor family in plants: a
RL genome-wide study of protein structure and functional diversity."
RL Mol. Biol. Evol. 20:735-747(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole plant;
RA Jakoby M.J., Heim M.A., Bailey P., Martin C., Weissshaar B.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; Z97336; CAB10220.1; -;
DR EMBL; AL161538; CAB78483.1; -;
DR EMBL; AF486628; AAM10963.1; -;
DR PIR; B71406; B71406.
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PSS0888; HLH; 1.
KW Hypothetical protein.
SQ SEQUENCE 277 AA; 31190 MW; 17D79957B8B77B48 CRC64;
Query Match 32.9%; Score 53; DB 2; Length 277;
Best Local Similarity 58.8%; Pred. No. 88;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 10 QHLDCCSRKCNFNKC 26
Db 106 EHLDDCCSRKARTGSC 122
RESULT 83
Q8L467 PRELIMINARY; PRT; 283 AA.
AC Q8L467
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AT4G14410/dl3245w (Hypothetical protein).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22088475; PubMed=12093376;
RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
RT "Full-length messenger RNA sequences greatly improve genome
RT annotation."
RL Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AY102106; AAM26676.1; -;
DR EMBL; AY088053; AAM65599.1; -;
DR EMBL; AY133565; AAM91395.1; -;
DR InterPro; IPR001092; HLH_basic.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR PROSITE; PSS0888; HLH; 1.
KW Hypothetical protein.
SQ SEQUENCE 283 AA; 31995 MW; AB758D25A07E12BB CRC64;
Query Match 32.9%; Score 53; DB 2; Length 283;
Best Local Similarity 58.8%; Pred. No. 89;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 10 QHLDCCSRKCNFNKC 26
Db 112 EHLDDCCSRKARTGSC 128
RESULT 84
Q44635 PRELIMINARY; PRT; 421 AA.
AC Q44635
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F16B4.9.
GN Name=F16B4.9; ORFNames=F16B4.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequencing of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Davidson S., Wohlmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid F16B4."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 23.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 21.
 DR PROSITE; PS00022; EGF_1; 33.
 DR PROSITE; PS01186; EGF_2; 25.
 DR PROSITE; PS50026; EGF_3; 35.
 DR PROSITE; PS01187; EGF_CA; 20.
 KW ANK repeat; EGF-like domain.
 SQ SEQUENCE 2531 AA; 273982 MW; 5BP42BEC627CA303 CRC64;
 Query Match 32.9%; Score 53; DB 2; Length 2531;
 Best Local Similarity 45.0%; Pred. No. 6.2e+02;
 Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 OY 8 CFQHLDDCCSRKGNFNKCV 27
 Db 662 CEEDIDDCSRPCHNGTCV 681
 RESULT 87
 NTCL_HUMAN
 ID_NTCL_HUMAN STANDARD; PRT; 2556 AA.
 AC P46531;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
 DE (translocation-associated notch protein TAN-1).
 GN Name=NOTCH1; Synonyms=TAN1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Mann R.S., Blaumueller C.M., Zagouras P.;
 RT "Complete human notch 1 (hnl) cDNA sequence";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-2444 FROM N.A.
 RX MEDLINE=91347367; PubMed=1831692; DOI=10.1016/0092-8674(91)90111-B;
 RA Ellisen L.W., Bird D., West D.C., Soreng A.L., Reynolds T.C.,
 RA Smith S.D., Sklar J.;
 RT "TAN-1, the human homolog of the Drosophila notch gene, is broken by
 RT chromosomal translocations in T lymphoblastic neoplasms.";
 RL Cell 66:649-661(1991).
 RN [3]
 RP IDENTIFICATION OF LIGANDS
 RX MEDLINE=99180745; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiades E., Henrique D., Carcangiu M.L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;
 RT "Human ligands of the Notch receptor";
 RL Am. J. Pathol. 154:785-794(1999).
 RN [4]
 RP INTERACTION WITH DTX1
 RX MEDLINE=98250176; PubMed=9590294;
 RA Matsuno K., Eastman D., Mitsiades T., Quinn A.M., Carcangiu M.L.,
 RA Ordentlich P., Kadesch T., Artavanis-Teakonas S.;
 RT "Human deltex is a conserved regulator of Notch signalling";
 RL Nat. Genet. 19:74-78(1998).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Deltal to regulate cell-face determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs. May be important for normal lymphocyte
 CC function. In altered form, may contribute to transformation or
 CC progression in some T-cell neoplasms. Involved in the maturation

of both CD4+ and CD8+ cells in the thymus (By similarity).
 -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity). Interacts with DTX1 and DTX2.
 -1- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus (By similarity).
 -1- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen, brain stem and lung. Also present in most adult tissues where it is found mainly in lymphoid tissues.
 -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in a trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
 -1- PTM: Phosphorylated (By similarity).
 -1- DISEASE: NOTCH1 truncation is associated with T-cell acute lymphoblastic leukemia.
 -1- SIMILARITY: Belongs to the NOTCH family.
 -1- SIMILARITY: Contains 5 ANK repeats.
 -1- SIMILARITY: Contains 36 EGF-like domains.
 -1- SIMILARITY: Contains 3 Lin/Notch repeats.

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 DR EMBL; AF308602; AAG33848.1; -.
 DR EMBL; M73980; AAA60614.1; -.
 DR PDB; 1PB5; NMR; A=1447-1481.
 DR Genew; HGNC:7881; NOTCH1.
 DR MIM; 190198; -.
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR010660; NOD.
 DR InterPro; IPR008297; Notch.
 DR InterPro; IPR000800; Notch_region.
 DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF00008; EGF; 35.
 DR Pfam; PF06816; NOD; 1.
 DR Pfam; PF00066; Notch; 3.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 23.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 20.
 DR PROSITE; PS00022; EGF_1; 34.
 DR PROSITE; PS01186; EGF_2; 26.
 DR PROSITE; PS50026; EGF_3; 36.
 DR PROSITE; PS01187; EGF_CA; 18.
 DR 3D-structure; Activator; ANK repeat; Developmental protein; Differentiation; EGF-like domain; Glycoprotein;


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AC Q646U5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytotoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RN SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
RT Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723722; AAU21463.1;
DR EMBL; AY723721; AAU21462.1;
SQ SEQUENCE 74 AA; 7702 MW; 294DCIA85D1D9FF0 CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 74;
Best Local Similarity 34.6%; Pred. No. 32;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
| : : : : : |
| : : : : : |
| : : : : : |
Db 47 CKAINAEVPA-FNDCCSKCNTGSPC 71

RESULT 90
Q646U7
ID Q646U7 PRELIMINARY; PRT; 74 AA.
AC Q646U7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Phytotoxin-like SCR74.
OS Phytophthora infestans (Potato late blight fungus).
OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
OC Phytophthora.
OX NCBI_TaxID=4787;
RN [1]
RN SEQUENCE FROM N.A.
RA Liu Z., Bos J.I.B., Armstrong M., Whisson S.C., da Cunha L.,
RA Torto-Alalibo T., Win J., Avrova A.O., Wright F., Birch P.R.J.,
RA Kamoun S.;
RT "Patterns of Diversifying Selection in the Phytotoxin-like scr74 Gene
RT Family of Phytophthora infestans.";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY723720; AAU21461.1;
SQ SEQUENCE 74 AA; 7802 MW; 57A8231D29AB5F8F CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 74;
Best Local Similarity 34.6%; Pred. No. 32;
Matches 9; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFNK 26
| : : : : : |
| : : : : : |
| : : : : : |
Db 47 CKAINAEVPA-FNDCCSKCNTGSPC 71

RESULT 91
Q6PV0
ID Q6PV0 PRELIMINARY; PRT; 92 AA.
AC Q6PV0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Egg protein CP422.
GN Names=CP422;
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

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OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RN SEQUENCE FROM N.A.
RA Yu C., Zhang F., Mihoko K., Masahiro I., Zhu Y., Hirayama K.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY570752; AAS68257.1;
SQ SEQUENCE 92 AA; 10345 MW; 052F01B53D379F5F CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 92;
Best Local Similarity 41.7%; Pred. No. 38;
Matches 10; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

Qy 1 CRXNQKCFQHLDDCCSRKCNRFN 24
| : : : : : |
| : : : : : |
| : : : : : |
Db 66 CLPDKQCCRRN-KDCCSKSCYRGN 88

RESULT 92
P93773
ID P93773 PRELIMINARY; PRT; 474 AA.
AC P93773;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 3-hydroxy-3-methylglutaryl-CoA-synthase.
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Needles;
RX MEDLINE=97214637; PubMed=9061017; DOI=10.1016/S0005-2760(96)00161-0;
RA Wegener A., Gimbel W., Werner T., Hani J., Ernst D., Sandermann H.;
RT "Molecular cloning of ozone-inducible protein from Pinus sylvestris L.
RT with high sequence similarity to vertebrate 3-hydroxy-3-methylglutaryl-
RT CoA-synthase.";
RL Biochim. Biophys. Acta 1350:247-252 (1997).
DR EMBL; X96386; CAA65250.1;
DR PIR; T09688; T09688.
DR GO; GO:0004421; F:hydroxymethylglutaryl-CoA synthase activity; IEA.
DR GO; GO:0006084; P:acetyl-CoA metabolism; IEA.
DR InterPro; IPR000886; ER target S.
DR InterPro; IPR008260; HMG CoA synth.
DR InterPro; IPR010122; HMG CoA S. euk.
DR Pfam; PF01154; HMG CoA synt.; 1.
DR TIGRFAMs; TIGR01833; HMG-CoA-S. euk.; 1.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN.1.
SQ SEQUENCE 474 AA; 52998 MW; 3ECB48E5F23D37BA CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 474;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 4 XNQKCF-QHLDDCCSRKCNRFNK 25
| : : : : : |
| : : : : : |
| : : : : : |
Db 211 LSQTCYLMALDSCYKFKCNKFEK 233

RESULT 93
Q6K5W7
ID Q6K5W7 PRELIMINARY; PRT; 764 AA.
AC Q6K5W7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative wall-associated kinase.
GN Name=P0016F11.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.

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OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AP005303; BAD22031.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004674; F:protein-serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR010881; EGF_Ca.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR008271; Ser Thr_pkinase.
DR Pfam; PF07645; EGF_CA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; Tyr_KG; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; UNKNOWN_1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 764 AA; 85266 MW; 5ECAB51B666C88C7 CRC64;

Query Match 32.6%; Score 52.5; DB 2; Length 764;
Best Local Similarity 26.2%; Pred. No. 2.5e+02;
Matches 11; Conservative 6; Mismatches 10; Indels 15; Gaps 2;

QY 1 CRXNKCQFQHLDDCCSRK--CNRFN-KC 27
DB 280 CRSTNSECFDTIDGQGVRCNCCQGVGNPYLDGCTDINECL 321

RESULT 94
SL17_ENTHI
ID SL17_ENTHI STANDARD; PRT; 1285 AA.
AC F23502;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE 170 kDa surface lectin precursor.
GN Name=CEL-170/4;
OS Entamoeba histolytica.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 16-33.
RX MEDLINE=91156704; PubMed=2000392;
RA Tannich E., Ebert F., Horstmann R.D.;
RT "Primary structure of the 170-kDa surface lectin of pathogenic
RT Entamoeba histolytica."
RL Proc. Natl. Acad. Sci. U.S.A. 88:1849-1853(1991).
RN [2]
RP REVISIONS TO N-TERMINUS.
RA Tannich E., Nickel R., Ebert F., Horstmann R.D.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 16-30.
RX MEDLINE=89123408; PubMed=2536731;
RA Petri W.A. Jr., Chapman M.D., Snodgrass T., Mann B.J., Broman J.,
RA Ravdin J.I.;
RT "Subunit structure of the galactose and N-acetyl-D-galactosamine-
RT inhibitable adherence lectin of Entamoeba histolytica."
RL J. Biol. Chem. 264:3007-3012(1989).
CC -!- FUNCTION: Mediates adherence of E. histolytica to colonic mucins,
CC an essential step for pathogenic tissue invasion.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Phosphorylated regions may have a role in signal

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transduction.
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EMBL; M60498; AAA32106.1; -.
EMBL; X61003; CA43321.1; -.
Direct protein sequencing; Glycoprotein; Lectin; Phosphorylation;
Repeat; Signal; Transmembrane.
FT SIGNAL 1 15
FT CHAIN 16 1285 170 kDa surface lectin.
FT DOMAIN 16 1218 Extracellular (Potential).
FT TRANSMEM 1219 1247 Potential.
FT DOMAIN 1248 1285 Cytoplasmic (Potential).
FT DOMAIN 378 1208 Cys-rich.
FT DOMAIN 378 653 9 x approximate tandem repeats.
FT REPEAT 378 407 1.
FT REPEAT 408 438 2.
FT REPEAT 439 464 3.
FT REPEAT 465 497 4.
FT REPEAT 498 525 5.
FT REPEAT 526 554 6.
FT REPEAT 555 584 7.
FT REPEAT 585 620 8.
FT REPEAT 621 653 9.
FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 236 236 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 330 330 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 383 383 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 651 651 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 882 882 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1196 1196 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1206 1206 N-linked (GlcNAc...) (Potential).
FT CONFLICT 16 16 D -> G (in Ref. 3).
SQ SEQUENCE 1285 AA; 144410 MW; 64BB2DFD2AD8ECBA CRC64;

Query Match 32.6%; Score 52.5; DB 1; Length 1285;
Best Local Similarity 41.4%; Pred. No. 3.9e+02;
Matches 12; Conservative 3; Mismatches 11; Indels 3; Gaps 2;

QY 1 CRXNKCQFQHLDDCCSRK--CNRFN-KC 26
DB 710 CSMGTDNVITYHDDCDRSKSCQGNFGKC 738

RESULT 95
Q9XV21
ID Q9XV21 PRELIMINARY; PRT; 354 AA.
AC Q9XV21;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F46B3.9.
DE ORFNames=F46B3.9;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none.
RT "genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
RN [2]

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DR PRINTS; PR01844; WNT4PROTEIN.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW Developmental protein; Glycoprotein; Lipoprotein; Palmitate; Signal;
KW Wnt signaling pathway.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 539 Wnt-4 protein.
FT CARBOHYD 74 74 N-linked (GLNac...) (Potential).
FT CARBOHYD 284 284 N-linked (GLNac...) (Potential).
FT CARBOHYD 419 419 N-linked (GLNac...) (Potential).
FT LIPID 274 274 S-palmitoyl cysteine (By similarity).
FT CONFLICT 18 18 F -> L (in Ref. 1).
FT CONFLICT 201 201 G -> R (in Ref. 1).
FT CONFLICT 230 230 F -> L (in Ref. 5).
FT CONFLICT 434 434 R -> A (in Ref. 1).
FT CONFLICT 532 532 L -> V (in Ref. 1).
SQ SEQUENCE 539 AA; 58685 MW; 6682C8B3D729D067 CRC64;

Query Match 26 32.3%; Score 52; DB 1; Length 539;
Best Local Similarity 39.1%; Pred. No. 2.1e+02;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps

Oy 1 CRXNQKCFQHLDDCCSRKNRF 23
|||::|::|::|::|::|::|:
Db 514 CFFNGRCCLICDYCORLENY 536
|||::|::|::|::|::|::|:

RESULT 98
Q9IBG4 PRELIMINARY; PRT; 778 AA.

ID	Q9IBG4	PRELIMINARY;	PRT;	778 AA.
AC	Q9IBG4;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Secretory protein containing EGF domain precursor.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]_TaxID=8355;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20245325; PubMed=10781962; DOI=10.1016/S0925-4773(00)00280-X;			
RA	Kuriyama S., Miyatani S., Kinoshita T.;			
RT	"XerI," a novel secretory protein expressed in eye and brain of Xenopus			
RT	embryo.";			
RL	Mech. Dev. 93:233-237(2000).			
DR	EMBL; AB027453; BAA95001.1; ..			
DR	HSPF; Q12780; IHAH.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0007155; P:cell adhesion; IEA.			
DR	InterPro; IPRO00152; Asx hydroxylase			
DR	InterPro; IPRO008985; Conk-like lec_gl.			
DR	InterPro; IPRO00742; EGF_2.			
DR	InterPro; IPRO01881; EGF Ca.			
DR	InterPro; IPRO01438; EGF II.			
DR	InterPro; IPRO06209; EGF like.			
DR	InterPro; IPRO09030; Grow fac recept.			
DR	InterPro; IPRO01791; Laminin_G.			
DR	InterPro; IPRO03129; TSP_N.			
DR	Pfam; PF00008; EGF; 12.			
DR	Pfam; PF02210; Laminin_G 2; 1.			
DR	PRINTS; PR00010; EGFBLOOD.			
DR	SMART; SM00179; EGF CA; 6.			
DR	SMART; SM00282; LamG; 1.			
DR	PROSITE; PS00010; ASX HYDROXYL; 7.			
DR	PROSITE; PS00022; EGF_1; 10.			
DR	PROSITE; PS01186; EGF_2; 10.			
DR	PROSITE; PS00026; EGF_3; 13.			
DR	PROSITE; PS01187; EGF CA; 6.			
DR	PROSITE; PS00025; LAM G DOMAIN; 1.			

DR GO: GO:0016327; C:apicolateral plasma membrane; IDA.
 DR GO: GO:0007163; P:establishment and/or maintenance of cell po. . . ; IMP.
 DR GO: GO:0016332; P:establishment and/or maintenance of polarit. . . ; IMP.
 DR GO: GO:0016334; P:establishment and/or maintenance of polarit. . . ; IMP.
 DR GO: GO:0002009; P:morphogenesis of an epithelium; NAS.
 DR GO: GO:0045494; P:photoreceptor maintenance; IMP.
 DR GO: GO:0042052; P:rhabdomere development; NAS.
 DR GO: GO:0045186; P:zonula adherens assembly; IMP.
 DR GO: GO:0045218; P:zonula adherens maintenance; IMP.
 DR InterPro: IPR000152; ASX_hydroxyl_S.
 DR InterPro: IPR008985; ConA_like_lec_gl.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF_II.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR001791; Laminin_G.
 DR Pfam: PF00008; EGF_26.
 DR Pfam: PF00054; Laminin_G_3.
 DR PRINTS: PR00054; Laminin_G.
 DR SMART: SM00179; EGF_BLOOD.
 DR SMART: SM00282; LamG_3.
 DR PROSITE: PS00010; ASX_HYDROXYL_15.
 DR PROSITE: PS00022; EGF_1_26.
 DR PROSITE: PS01186; EGF_2_17.
 DR PROSITE: PS50026; EGF_3_27.
 DR PROSITE: PS01187; EGF_Ca_12.
 DR PROSITE: PS50025; LAM_G_DOMAIN_3.
 KW Differentiation; EGF-like domain; Glycoprotein; Phosphorylation;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 90
 FT CHAIN 91 2139
 FT DOMAIN 91 2084 Crumbs protein.
 FT TRANSMEM 2085 2111 Extracellular (Potential).
 FT DOMAIN 2112 2139 Potential.
 FT DOMAIN 267 303 Cytoplasmic (Potential).
 FT DOMAIN 306 343 EGF-like 1.
 FT DOMAIN 348 386 EGF-like 2.
 FT DOMAIN 388 425 EGF-like 3.
 FT DOMAIN 427 463 EGF-like 4, calcium-binding (Potential).
 FT DOMAIN 464 500 EGF-like 5.
 FT DOMAIN 501 532 EGF-like 6.
 FT DOMAIN 545 581 EGF-like 7.
 FT DOMAIN 582 611 EGF-like 8.
 FT DOMAIN 609 646 EGF-like 9.
 FT DOMAIN 648 685 EGF-like 10.
 FT DOMAIN 687 723 EGF-like 11, calcium-binding (Potential).
 FT DOMAIN 725 761 EGF-like 12, calcium-binding (Potential).
 FT DOMAIN 763 800 EGF-like 13, calcium-binding (Potential).
 FT DOMAIN 802 838 EGF-like 14, calcium-binding (Potential).
 FT DOMAIN 840 902 EGF-like 15, calcium-binding (Potential).
 FT DOMAIN 904 940 EGF-like 16.
 FT DOMAIN 942 978 EGF-like 17, calcium-binding (Potential).
 FT DOMAIN 980 1021 EGF-like 18, calcium-binding (Potential).
 FT DOMAIN 1023 1205 EGF-like 19.
 FT DOMAIN 1207 1243 Laminin G-like 1.
 FT DOMAIN 1250 1480 EGF-like 20.
 FT DOMAIN 1481 1517 Laminin G-like 2.
 FT DOMAIN 1558 1758 EGF-like 21.
 FT DOMAIN 1759 1795 Laminin G-like 3.
 FT DOMAIN 1797 1833 EGF-like 22.
 FT DOMAIN 1835 1871 EGF-like 23, calcium-binding (Potential).
 FT DOMAIN 1874 1915 EGF-like 24, calcium-binding (Potential).
 FT DOMAIN 1915 1951 EGF-like 25.
 FT DOMAIN 1953 1989 EGF-like 26.
 FT DOMAIN 1991 2029 EGF-like 27, calcium-binding (Potential).
 FT DOMAIN 2030 2070 EGF-like 28, calcium-binding (Potential).
 FT DOMAIN 2070 2139 EGF-like 29.
 FT DISULFID 271 282 By similarity.
 FT DISULFID 276 291 By similarity.
 FT DISULFID 293 302 By similarity.
 FT DISULFID 310 321 By similarity.
 FT DISULFID 315 331 By similarity.
 FT DISULFID 333 342 By similarity.
 FT DISULFID 352 363 By similarity.

FT DISULFID 357 374 By similarity.
 FT DISULFID 376 385 By similarity.
 FT DISULFID 392 403 By similarity.
 FT DISULFID 397 412 By similarity.
 FT DISULFID 414 424 By similarity.
 FT DISULFID 431 442 By similarity.
 FT DISULFID 436 451 By similarity.
 FT DISULFID 453 462 By similarity.
 FT DISULFID 468 479 By similarity.
 FT DISULFID 473 488 By similarity.
 FT DISULFID 490 499 By similarity.
 FT DISULFID 505 515 By similarity.
 FT DISULFID 509 520 By similarity.
 FT DISULFID 522 531 By similarity.
 FT DISULFID 549 562 By similarity.
 FT DISULFID 556 569 By similarity.
 FT DISULFID 571 580 By similarity.
 FT DISULFID 586 597 By similarity.
 FT DISULFID 591 602 By similarity.
 FT DISULFID 604 610 By similarity.
 FT DISULFID 613 624 By similarity.
 FT DISULFID 636 645 By similarity.
 FT DISULFID 652 664 By similarity.
 FT DISULFID 659 673 By similarity.
 FT DISULFID 675 684 By similarity.
 FT DISULFID 691 702 By similarity.
 FT DISULFID 696 711 By similarity.
 FT DISULFID 713 722 By similarity.

Query Match 32.3%; Score 52; DB 1; Length 2139;
 Best Local Similarity 30.4%; Pred. No. 7.1e+02;
 Matches 7; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 4 XNQCFOHLDCCSRKCNRFNC 26
 DB 1828 EGQHCQNIIDCADQPCCHNGNC 1850

Search completed: April 18, 2005, 20:37:49
 Job time : 120 secs